

SEQUENCE LISTING

- <110> Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
- <120> Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
- <130> 10466-14
- <140> 09/665,350
<141> 2000-09-18
- <150> PCT/US00/04414
<151> 2000-02-22
- <150> US 60/143,048
<151> 1999-07-07
- <150> US 60/145,698
<151> 1999-07-26
- <150> US 60/146,222
<151> 1999-07-28
- <150> PCT/US99/20594
<151> 1999-09-08
- <150> PCT/US99/20944
<151> 1999-09-13

<150> PCT/US99/21090
<151> 1999-09-15

<150> PCT/US99/21547
<151> 1999-09-15

<150> PCT/US99/23089
<151> 1999-10-05

<150> PCT/US99/28214
<151> 1999-11-29

<150> PCT/US99/28313
<151> 1999-11-30

<150> PCT/US99/28564
<151> 1999-12-02

<150> PCT/US99/28565
<151> 1999-12-02

<150> PCT/US99/30095
<151> 1999-12-16

<150> PCT/US99/30911
<151> 1999-12-20

<150> PCT/US99/30999
<151> 1999-12-20
<150> PCT/US00/00219
<151> 2000-01-05

<160> 423

<210> 1
<211> 1825
<212> DNA
<213> Homo sapiens

<400> 1
actgcacctc ggttctatcg attgaattcc ccgggggatcc tctagagatc cctcgacctc 60
gacccacgcg tccggggccgg agcagcacgg ccgcaggacc tggagctccg gctgcgtctt 120
cccgcagcgc taccgcccat gcgcctgccg ccggggggccg cgctgggggt cctgccgctt 180
ctgctgctgc tgccgcccgc gccggaggcc gccaaagaagc cgacgccttg ccaccggtgc 240
cgggggctgg tggacaagtt taaccagggg atggtggaca ccgcaaagaa gaactttggc 300
ggcgggaaca cggcttgagg ggaagagacg ctgtccaagt acgagtccag cgagattcgc 360
ctgctggaga tcctggaggg gctgtgagag agcagcgact tcgaatgcaa tcagatgcta 420
gaggcgaggg agggagcacct ggaggcctgg tggctgcagc tgaagagcga atatcctgac 480
ttattcgagt ggttttgtgt gaagacactg aaagtgtgct gctctccagg aacctacggc 540
cccgactgtc tcgcatgcca gggcggatcc cagaggccct gcagcgggaa tggccactgc 600
agcggagatg ggagcagaca gggcgacggg tcctgcccgt gccacatggg gtaccagggc 660

```
<210> 2
<211> 353
<212> PRT
<213> Homo sapiens
```

```

<400> 2
Met Arg Leu Pro Arg Arg Ala Ala Leu Gly Leu Leu Pro Leu Leu Leu
  1              5              10              15

Leu Leu Pro Pro Ala Pro Glu Ala Ala Lys Lys Pro Thr Pro Cys His
      20              25              30

Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
      35              40              45

Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
      50              55              60

Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
  65              70              75              80

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
      85              90              95

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
      100              105              110

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
      115              120              125

Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
      130              135              140

```

Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg
 145 150 155 160
 Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu
 165 170 175
 Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr
 180 185 190
 His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly
 195 200 205
 Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp
 210 215 220
 Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
 225 230 235 240
 Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys
 245 250 255
 Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly
 260 265 270
 Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys
 275 280 285
 Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys
 290 295 300
 Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro
 305 310 315 320
 Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys Val Pro Pro Ala Glu Ala
 325 330 335
 Glu Ala Thr Glu Gly Glu Ser Pro Thr Gln Leu Pro Ser Arg Glu Asp
 340 345 350
 Leu

<210> 3
 <211> 2206
 <212> DNA
 <213> Homo sapiens

<400> 3
 caggtccaac tgcacctcgg ttctatcgat tgaattcccc ggggatacctc tagagatccc 60
 tcgacctcga cccacgcgtc cgccaggccg ggaggcgacg cgcccagccg tctaaacggg 120
 aacagccctg gctgagggag ctgcagcgca gcagagtatc tgacggcgcc aggttgcgta 180
 ggtgcggcac gaggagtttt cccggcagcg aggaggtcct gagcagcatg gcccgaggga 240


```

gcgccttccc tgcgcgcgcg ctctggctct ggagcctcct cctgtgcctg ctggcactgc 300
gggcgagggc cgggcccgcg caggaggaga gcctgtacct atggatcgat gctcaccagg 360
caagagtact cataggattt gaagaagata tcctgattgt ttcagagggg aaaatggcac 420
cttttacaca tgatttcaga aaagcgcaac agagaatgcc agctattcct gtcaatatcc 480
attccatgaa ttttacctgg caagctgcag ggcaggcaga atacttctat gaattcctgt 540
ccttgcgctc cctggataaa ggcacatgag cagatccaac cgtcaatgtc cctctgctgg 600
gaacagtgcc tcacaaggca tcagttgttc aagttggttt cccatgtctt ggaaaacagg 660
atgggggtggc agcatttgaa gtggatgtga ttgttatgaa ttctgaaggc aacaccattc 720
tccaaacacc tcaaaatgct atcttcttta aaacatgtca acaagctgag tggccaggcg 780
ggtgccgaaa tggaggcttt tgtaatgaaa gacgcactct cgagtgtcct gatgggttcc 840
acggacctca ctgtgagaaa gccctttgta cccacgatg tatgaatggt ggactttgtg 900
tgactcctgg tttctgcac tggccacctg gattctatgg agtgaactgt gacaaagcaa 960
actgctcaac cacctgcttt aatggaggga cctgtttcta cctggaaaa tgtatttgcc 1020
ctccaggact agagggagag cagtgtgaaa tcagcaaattg cccacaaccc tgtcgaaatg 1080
gaggtaaatg cattggtaaa agcaaattga agtgttccaa aggttaccag ggagacctct 1140
gttcaaagcc tgtctgcgag cctggctgtg gtgcacatgg aacctgccat gaacccaaca 1200
aatgccaatg tcaagaaggt tggcatggaa gacactgcaa taaaaggtag gaagccagcc 1260
tcatacatgc cctgaggcca gcaggcgccc agctcaggca gcacacgctt tactttaaaa 1320
aggccgagga gggcggggat ccacctgaat ccaattacat ctggtgaact ccgacatctg 1380
aaacgtttta agttacacca agttcatagc ctttggttaac ctttcatgtg ttgaatgttc 1440
aaataatggt cattacactt aagaatactg gcctgaattt tattagcttc attataaatc 1500
actgagctga tatttactct tccttttaag ttttctaagt acgtctgtag catgatggta 1560
tagattttct tgtttcagtg ctttgggaca gattttatat tatgtcaatt gatcaggtta 1620
aaattttcag tgtgtagttg gcagatattt tcaaaattac aatgcattta tgggtgtctg 1680
gggcagggga acatcagaaa ggttaaattg ggcaaaaatg cgtaagtcac aagaatttgg 1740
atggtgcagt taatgttgaa gttacagcat ttcagatttt attgtcagat atttagatgt 1800
ttgttacatt tttaaaaatt gctcttaatt tttaaactct caatacaata tattttgacc 1860
ttaccattat tccagagatt cagtattaaa aaaaaaaaaa ttactctgtg gtatggcat 1920
ttaaacaata taatatattc taaacacaat gaaataggga atataatgta tgaacttttt 1980
gcattggctt gaagcaatat aatatattgt aaacaaaaca cagctcttac ctaataaaca 2040
ttttatactg tttgtatgta taaaataaag gtgctgcttt agtttttttg aaaaaaaaaa 2100
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gggcgggcgc gactctagag tcgacctgca 2160
gaagcttggc cgccatggcc caacttgttt attgcagctt ataattg 2206

```

```

<210> 4
<211> 379
<212> PRT
<213> Homo sapiens

```

```

<400> 4
Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp Ser
  1              5              10              15

Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln
      20              25              30

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
      35              40              45

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
      50              55              60

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

```

65				70				75				80			
Pro	Val	Asn	Ile	His	Ser	Met	Asn	Phe	Thr	Trp	Gln	Ala	Ala	Gly	Gln
				85					90					95	
Ala	Glu	Tyr	Phe	Tyr	Glu	Phe	Leu	Ser	Leu	Arg	Ser	Leu	Asp	Lys	Gly
			100					105				110			
Ile	Met	Ala	Asp	Pro	Thr	Val	Asn	Val	Pro	Leu	Leu	Gly	Thr	Val	Pro
		115					120					125			
His	Lys	Ala	Ser	Val	Val	Gln	Val	Gly	Phe	Pro	Cys	Leu	Gly	Lys	Gln
	130					135					140				
Asp	Gly	Val	Ala	Ala	Phe	Glu	Val	Asp	Val	Ile	Val	Met	Asn	Ser	Glu
145					150					155					160
Gly	Asn	Thr	Ile	Leu	Gln	Thr	Pro	Gln	Asn	Ala	Ile	Phe	Phe	Lys	Thr
			165						170					175	
Cys	Gln	Gln	Ala	Glu	Cys	Pro	Gly	Gly	Cys	Arg	Asn	Gly	Gly	Phe	Cys
			180					185					190		
Asn	Glu	Arg	Arg	Ile	Cys	Glu	Cys	Pro	Asp	Gly	Phe	His	Gly	Pro	His
		195					200					205			
Cys	Glu	Lys	Ala	Leu	Cys	Thr	Pro	Arg	Cys	Met	Asn	Gly	Gly	Leu	Cys
	210					215					220				
Val	Thr	Pro	Gly	Phe	Cys	Ile	Cys	Pro	Pro	Gly	Phe	Tyr	Gly	Val	Asn
225					230					235					240
Cys	Asp	Lys	Ala	Asn	Cys	Ser	Thr	Thr	Cys	Phe	Asn	Gly	Gly	Thr	Cys
				245					250					255	
Phe	Tyr	Pro	Gly	Lys	Cys	Ile	Cys	Pro	Pro	Gly	Leu	Glu	Gly	Glu	Gln
			260					265					270		
Cys	Glu	Ile	Ser	Lys	Cys	Pro	Gln	Pro	Cys	Arg	Asn	Gly	Gly	Lys	Cys
		275					280					285			
Ile	Gly	Lys	Ser	Lys	Cys	Lys	Cys	Ser	Lys	Gly	Tyr	Gln	Gly	Asp	Leu
	290					295					300				
Cys	Ser	Lys	Pro	Val	Cys	Glu	Pro	Gly	Cys	Gly	Ala	His	Gly	Thr	Cys
305					310					315					320
His	Glu	Pro	Asn	Lys	Cys	Gln	Cys	Gln	Glu	Gly	Trp	His	Gly	Arg	His
				325					330					335	
Cys	Asn	Lys	Arg	Tyr	Glu	Ala	Ser	Leu	Ile	His	Ala	Leu	Arg	Pro	Ala
			340					345					350		

<400> 8
ccacgatgt atgaatggtg gactttgtgt gactcctggt ttctgcac 49

<210> 9
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 9
 aaagacgcat ctgagtggt cc 22

<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 10
 tgctgatttc acactgctct ccc 23

<210> 11
 <211> 2197
 <212> DNA
 <213> Homo sapiens

<400> 11
 cggacgcgtg ggcgtccggc ggtcgcagag ccaggaggcg gaggcgcgcg ggccagcctg 60
 ggccccagcc cacaccttca ccagggccca ggagccacca tgtggcgatg tccactgggg 120
 ctactgctgt tgctgccgtt ggctggccac ttggctcttg gtgcccagca gggctcgtggg 180
 cgccggggagc tagcaccggg tctgcacctg cggggcatcc gggacgcggg aggccgggtac 240
 tgccaggagc aggcacctgt ctgccgcggc cgtgccgacg actgtgccct gccctacctg 300
 ggcgccatct gttactgtga cctcttctgc aaccgcacgg tctccgactg ctgccctgac 360
 ttctgggact tctgcctcgg cgtgccaccc ccttttcccc cgatccaagg atgtatgcat 420
 ggaggtcgta tctatccagt cttgggaacg tactgggaca actgtaaccg ttgcacctgc 480
 caggagaaca ggcagtggca tgggtggatcc agacatgac aaagccatca accagggcaa 540
 ctatggctgg caggctggga accacagcgc cttctggggc atgacctgg atgagggcat 600
 tcgctaccgc ctgggcacca tccgcccatc ttctcgggtc atgaacatgc atgaaattta 660
 tacagtgtct aaccagggg aggtgcttcc cacagccttc gaggcctctg agaagtggcc 720
 caacctgatt catgagcctc ttgaccaagg caactgtgca ggctcctggg ccttctccac 780
 agcagctgtg gcatccgac gtgtctcaat ccattctctg ggacacatga cgcctgtcct 840
 gtgcgccag aacctgctgt cttgtgacac ccaccagcag cagggtgcc gcggtggggc 900
 tctcgatggt gcctggtggt tctgcgtcg ccgaggggtg gtgtctgacc actgctaccc 960
 cttctcgggc cgtgaacgag acgaggctgg cctgcgccc cctgtatga tgcacagccg 1020
 agccatgggt cggggcaagc gccaggccac tgcccactgc cccaacagct atgttaataa 1080
 caatgacatc taccaggtca ctctgtcta ccgctcggc tccaacgaca aggagatcat 1140
 gaaggagctg atggagaatg gccctgtcca agcctcatg gaggtgcatg aggacttctt 1200
 cctatacaag ggaggcatct acagccacac gccagtgagc cttgggaggc cagagagata 1260
 ccgccggcat gggaccact cagtcaagat cacaggatgg ggagaggaga cgctgccaga 1320

```
<210> 12
<211> 164
<212> PRT
<213> Homo sapiens
```

```

<400> 12
Met Trp Arg Cys Pro Leu Gly Leu Leu Leu Leu Leu Pro Leu Ala Gly
  1                      5                      10                      15

His Leu Ala Leu Gly Ala Gln Gln Gly Arg Gly Arg Arg Arg Glu Leu Ala
      20                      25                      30

Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
      35                      40                      45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
      50                      55                      60

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr
  65                      70                      75                      80

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro
      85                      90                      95

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr
      100                      105                      110

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
      115                      120                      125

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln
      130                      135                      140

Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly
  145                      150                      155                      160

His Asp Pro Gly

```

<210> 13
 <211> 533
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (33)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (80)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (94)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (144)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (188)
 <223> a, t, c or g

<400> 13
 aggctccttg gccctttttc cacagcaagc ttntgcnatc ccgattcggt gtctcaaatac 60
 caattctctt gggacacatn acgcctgtcc tttngcccca gaacctgctg tcttgtacac 120
 ccaccagcag cagggctgcc gcgntgggag tctcgatggg gcctgggtgg tcttgcgtcg 180
 ccgagggntg gtgtctgacc actgctaccc cttctcgggc cgtgaacgag acgaggctgg 240
 ccctgcgccc ccctgtatga tgcacagccg agccatgggt cggggcaagc gccaggccac 300
 tgcccactgc cccaacagct atgttaataa caatgacatc taccaggtca ctctgtcta 360
 ccgcctcggc tccaacgaca aggagatcat gaaggagctg atggagaatg gccctgtcca 420
 agccctcatg gaggtgcatg aggacttctt cctatacaag ggaggcatct acagccacac 480
 gccagtgagc cttgggaggc cagagagata ccgccggcat gggaccact cag 533

<210> 14
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 14

ttcgaggcct ctgagaagtg gccc

24

<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 15

ggcggtatct ctctggcctc cc

22

<210> 16

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 16

ttctccacag cagctgtggc atccgatcgt gtctcaatcc attctctggg

50

<210> 17

<211> 960

<212> DNA

<213> Homo sapiens

<400> 17

gctgcttgcc ctgttgatgg caggcttgcc cctgcagcca ggcaactgccc tgctgtgcta 60
ctcctgcaaa gccaggtga gcaacgagga ctgcctgcag gtggagaact gcacccagct 120
gggggagcag tgctggaccg cgcgcattcc cgcagttggc ctctgaccg tcatcagcaa 180
aggctgcagc ttgaactgcg tggatgactc acaggactac tacgtgggca agaagaacat 240
cacgtgctgt gacaccgact tgtgcaacgc cagcggggcc catgccctgc agccggctgc 300
cgccatcctt gcgctgctcc ctgcactcgg cctgctgctc tggggaccgc gccagctata 360
ggctctgggg ggccccgctg cagccacac tgggtgtggg gccccaggcc tctgtgccac 420
tcctcacaga cctggcccag tgggagcctg tcctggttcc tgaggcacat cctaacgcaa 480
gtctgacat gtatgtctgc acccctgtcc cccaccctga ccctcccatg gccctctcca 540
ggactccac ccggcagatc agctctagt acacagatcc gcctgcagat ggccccctcca 600
accctctctg ctgctgtttc catggcccag cattctccac ccttaaccct gtgctcaggc 660
acctcttccc ccaggaagcc ttccctgccc accccatcta tgacttgagc cagggtctgg 720
ccgtggtgtc ccccgaccc agcaggggac aggcactcag gagggcccag taaaggctga 780
gatgaagtgg actgagtaga actggaggac aagagtcgac gtgagtctct gggagtctcc 840
agagatgggg cctggaggcc tggaggaagg ggccaggcct cacattcgtg gggctccttg 900
aatggcagcc tgagcacagc gtaggccctt aataaacacc tgttgataa gccaaaaaaa 960

<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

11

<400> 18

Met Thr His Arg Thr Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val
 1 5 10 15

Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu
 20 25 30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp
 35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly
 50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp
 65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met
 85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser
 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala
 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe
 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe
 145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser
 165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln
 180 185

<210> 19

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 19

tgctgtgcta ctctgcaaa gccc

24

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 20

tgcacaagtc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 21

agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

```

cccacgcgtc cgaacctctc cagcgatggg agccgcccgc ctgctgccc aacctactct 60
gtgcttacag ctgctgattc tctgctgtca aactcagtac gtgagggacc agggcgccat 120
gaccgaccag ctgagcaggc ggcagatccg cgagtaccaa ctctacagca ggaccagtgg 180
caagcacgtg caggtcaccg ggcgtcgcat ctccgccacc gccgaggacg gcaacaagtt 240
tgccaagctc atagtggaga cggacacgtt tggcagccgg gttcgcatca aaggggctga 300
gagtgagaag tacatctgta tgaacaagag gggcaagctc atcggaagc ccagcgggaa 360
gagcaaagac tgcgtgttca cggagatcgt gctggagaac aactatacgg ccttccagaa 420
cgcccggcac gagggctggg tcatggcctt cacgcggcag gggcgggccc gccaggcttc 480
ccgcagccgc cagaaccagc gcgaggccca ctcatcaag cgcctctacc aaggccagct 540
gcccttcccc aaccacgccg agaagcagaa gcagttcgag tttgtgggct ccgccccac 600
ccgcccggacc aagcgcacac ggcggcccca gcccctcag tagtctggga ggcagggggc 660
agcagcccct gggccgcctc cccaccctt tcccttctta atccaaggac tgggctgggg 720
tggcgggagg ggagccagat ccccgagga ggaccctgag ggccgcgaag catccgagcc 780
cccagctggg aaggggcagg ccggtgcccc aggggcggct ggcacagtgc ccccttcccc 840
gacgggtggc aggcctgga gaggaactga gtgtcaccct gatctcaggc caccagctc 900
tgccggcctc ccagccgggc tctgaagcc cgctgaaagg tcagcgactg aaggccttgc 960
agacaaccgt ctggaggtgg ctgtcctcaa aatctgcttc tcggatctcc ctgagtctgc 1020
ccccagcccc caaactcctc ctggctagac tgtaggaagg gacttttgtt tgtttgtttg 1080
tttcaggaaa aaagaaaggg agagagagga aaatagaggg ttgtccactc ctcacattcc 1140
acgaccagc cctgcacccc accccaact cccagccccg gaataaaacc attttctctgc 1200

```

<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

<400> 23

Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu
 1 5 10 15

Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met
 20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser
 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn
 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr
 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr
 195 200 205

<210> 24

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 24

cagtacgtga gggaccaggg cgccatga

28

<210> 25

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 25
 ccggtgacct gcacgtgctt gccca

24

<210> 26
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<220>
 <221> modified_base
 <222> (21)
 <223> a, t, c or g

<400> 26
 gcggatctgc cgctgctca nctggtcggt catggcgccc t

41

<210> 27
 <211> 2479
 <212> DNA
 <213> Homo sapiens

<400> 27
 atttgccatc acctgttgcc agtgtggaaa aattctccct gttgaatttt ttgcacatgg 60
 aggacagcag caaagagggc aacacagget gataagacca gagacagcag ggagattatt 120
 ttaccatacg cctcaggac gttccctcta gctggagttc tggacttcaa cagaacccca 180
 tccagtcatt ttgattttgc tgtttatttt ttttttcttt ttctttttcc caccacattg 240
 tatttttatt ccgtacttca gaaatgggccc tacagaccac aaagtggccc agccatgggg 300
 cttttttcct gaagtcttgg cttatcattt ccctggggct ctactcacag gtgtccaaac 360
 tcctggcctg ccctagtgtg tgccgctgcg acaggaactt tgtctactgt aatgagcgaa 420
 gcttgacctc agtgcctctt gggatcccgg agggcgtaac cgtactctac ctccacaaca 480
 accaaattaa taatgctgga tttcctgcag aactgcacaa tgtacagtcg gtgcacacgg 540
 tctacctgta tggcaaccaa ctggacgaat tccccatgaa ccttcccaag aatgtcagag 600
 ttctccattt gcaggaaaac aatattcaga ccatttcaag ggctgctctt gccagctct 660
 tgaagcttga agagctgcac ctggatgaca actccatata cacagtgggg gtggaagacg 720
 gggccttccg ggaggctatt agcctcaaat tgttggtttt gtctaagaat cacctgagca 780
 gtgtgcctgt tgggcttctt gtggacttgc aagagctgag agtggatgaa aatcgaattg 840
 ctgtcatatc cgacatggcc ttccagaatc tcacgagctt ggagcgtctt attgtggacg 900
 ggaacctcct gaccaacaag ggtatcgccg agggcacctt cagccatctc accaagctca 960
 aggaattttc aattgtacgt aattcgctgt cccaccctcc tcccgatctc ccagggtacg 1020
 atctgatcag gctctatttg caggacaacc agataaacca cattcctttg acagccttct 1080
 caaatctgcg taagctggaa cggctggata tatccaacaa ccaactgcgg atgctgactc 1140

```

aagggggttt tgataatctc tccaacctga agcagctcac tgctcggaat aacccttggt 1200
tttgtgactg cagtattaaa tgggtcacag aatgggtcaa atatatccct tcatctctca 1260
acgtgcgggg tttcatgtgc caaggctctg aacaagtccg ggggatggcc gtcaggggaat 1320
taaatatgaa tcttttgtcc tgtcccacca cgaccccccg cctgcctctc ttcaccccag 1380
ccccaagtac agcttctccg accactcagc ctcccacct ctctattcca aaccctagca 1440
gaagctacac gcctccaact cctaccacat cgaaacttcc cagcattcct gactgggatg 1500
gcagagaaaag agtgacccca cctatttctg aacggatcca gctctctatc cattttgtga 1560
atgatacttc cattcaagtc agctggctct ctctcttcac cgtgatggca taaaaactca 1620
catgggtgaa aatggggccac agtttagtag ggggcatcgt tcaggagcgc atagtcagcg 1680
gtgagaagca acacctgagc ctggttaact tagagccccg atccacctat cggatttggt 1740
tagtgccact gtagtctttt aactaccgcg cggtagaaga caccatttgt tcagaggcca 1800
ccacccatgc ctctatctg aacaacggca gcaacacagc gtccagccat gagcagacga 1860
cgtcccacag catggggtcc ccctttctgc tggcgggctt gatcgggggc gcggtgatat 1920
ttgtgctggt ggtcttgctc agcgtctttt gctggcatat gcacaaaaag gggcgctaca 1980
cctcccagaa gtggaaatac aaccggggcc ggcggaaaga tgattattgc gaggcaggca 2040
ccaagaagga caactccatc ctggagatga cagaaaccag ttttcagatc gtctccttaa 2100
ataacgatca actccttaaa ggagatttca gactgcagcc catttacacc ccaaattggg 2160
gcattaatta cacagactgc catatcccca acaacatgcg atactgcaac agcagcgtgc 2220
cagacctgga gcaactgccat acgtgacagc cagaggccca gcgttatcaa ggcggacaat 2280
tagactcttg agaacacact cgtgtgtgca cataaagaca cgcagattac atttgataaa 2340
tgttacacag atgcatttgt gcatttgaat actctgtaat ttatacgggtg tactatataa 2400
tgggatttaa aaaaagtgtc atcttttcta tttcaagtta attacaaaca gttttgtaac 2460
tctttgcttt ttaaattctt                                     2479

```

<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu

1 5 10 15

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys

20 25 30

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr

35 40 45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly

50 55 60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe

65 70 75 80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr

85 90 95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg

100 105 110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala

115 120 125

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser
 130 135 140
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser
 145 150 155 160
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val
 165 170 175
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile
 180 185 190
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg
 195 200 205
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly
 210 215 220
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn
 225 230 235 240
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg
 245 250 255
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe
 260 265 270
 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu
 275 280 285
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln
 290 295 300
 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp
 305 310 315 320
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly
 325 330 335
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu
 340 345 350
 Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro
 355 360 365
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro
 370 375 380
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro
 385 390 395 400
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

405 410 415
 Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val
 420 425 430
 Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met
 435 440 445
 Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly
 450 455 460
 Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu
 465 470 475 480
 Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu
 485 490 495
 Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala
 500 505 510
 Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser
 515 520 525
 His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala
 530 535 540
 Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser
 545 550 555 560
 Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys
 565 570 575
 Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly
 580 585 590
 Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln
 595 600 605
 Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu
 610 615 620
 Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His
 625 630 635 640
 Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu
 645 650 655
 His Cys His Thr
 660

<210> 29
 <211> 21
 <212> DNA

<220>

<400> 29

21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<400> 30

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<400> 31

22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<400> 32

46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

acttggagca agcggcggcg gcggagacag aggcagaggc agaagctggg gctccgtcct 60
cgctcccac gagcgatccc cgaggagagc cgcggccctc ggcgaggcga agaggccgac 120

```

gaggaagacc cgggtggctg cggccctgcc tcgttccca ggcgcggcg gctgcagcct 180
tgccctctt gctcgcttg aaaatggaaa agatgctcgc aggtgcttt ctgctgatcc 240
tcggacagat cgtcctctc cctgccgagg ccaggagcg gtcacgtggg aggtccatct 300
ctaggggag acacgctcgg acccaccgc agacggcct tctggagagt tctgtgaga 360
acaagcgggc agacctggtt ttcattctg acagctctcg cagtgtcaac acccatgact 420
atgcaaaggc caaggagttc atcgtggaca tcttgcaatt cttggacatt ggtcctgatg 480
tcacccgagt gggcctgctc caatatggca gcaactgtca gaatgagttc tccctcaaga 540
ccttcaagag gaagtccgag gtggagcgtg ctgtcaagag gatgcggcat ctgtccacgg 600
gcaccatgac tgggctggcc atccagtatg cctgaacat cgcattctca gaagcagagg 660
gggcccggcc cctgagggag aatgtgccac gggtcataat gatcgtgaca gatgggagac 720
ctcaggactc cgtggccgag gtggctgcta aggcacggga cacgggcac ctaatctttg 780
ccattggtgt gggccaggta gacttcaaca ccttgaagtc cattgggagt gacccccatg 840
aggaccatgt ctcccttggt gccaatttca gccagattga gacgctgacc tccgtgttcc 900
agaagaagtt gtgcacggcc cacatgtgca gcaccctgga gcataactgt gccacttct 960
gcatcaacat cctgggtca tacgtctgca ggtgcaaca aggtacatt ctcaactcgg 1020
atcagacgac ttgcagaatc caggatctgt gtgccatgga ggaccacaac tgtgagcagc 1080
tctgtgtgaa tgtgccgggc tcttcgtct gccagtgcta cagtggctac gccctggctg 1140
aggatgggaa gaggtgtgtg gctgtggact actgtgcctc agaaaaccac ggatgtgaac 1200
atgagtgtgt aaatgctgat ggctcctacc tttgccagtg ccatgaagga tttgctctta 1260
accagatga aaaaacgtgc acaaggatca actactgtgc actgaacaaa ccgggctgtg 1320
agcatgagtg cgtcaacatg gaggagagct actactgccg ctgccaccgt ggctacactc 1380
tggaccccaa tggcaaaacc tgcagccgag tggaccactg tgcacagcag gaccatggct 1440
gtgagcagct gtgtctgaac acggaggatt ccttcgtctg ccagtgtca gaaggttcc 1500
tcatcaacga ggacctcaag acctgctccc ggggtggatta ctgctgctg agtgaccatg 1560
gttgtgaata ctctgtgtc aacatggaca gatcctttgc ctgtcagtgt cctgagggac 1620
acgtgctccg cagcgtggg aagacgtgtg caaatctgga ctctgtgtc ctgggggacc 1680
acggttgtga acattcgtgt gtaagcagtg aagattcgtt tgtgtgccag tgccttgaag 1740
gttatatact ccgtgaagat ggaaaaacct gcagaaggaa agatgtctgc caagctatag 1800
accatggctg tgaacacatt tgtgtgaaca gtgacgactc atacacgtgc gagtgttgg 1860
agggattccg gctcgtgag gatgggaaac gctgccgaag gaaggatgtc tgcaaatcaa 1920
cccaccatgg ctgcaaacac atttgtgtta ataatgggaa ttctacatc tgcaaatgct 1980
cagagggatt tgttctagct gaggacggaa gacgggtgca gaaatgact gaaggcccaa 2040
ttgacctggt ctttgtgatc gatggatcca agagtcttg agaagagaat tttgaggtcg 2100
tgaagcagtt tgtcactgga attatagatt ccttgacaat tcccccaaa gccgctcgag 2160
tggggctgct ccagtattcc acacaggtcc acacagagtt cactctgaga aacttcaact 2220
cagccaaaga catgaaaaaa gccgtggccc acatgaaata catgggaaag ggctctatga 2280
ctgggctggc cctgaaacac atgtttgaga gaagttttac ccaaggagaa ggggccaggc 2340
ccctttccac aagggtgccc agagcagcca ttgtgttcac cgacggacgg gctcaggatg 2400
acgtctccga gtgggccagt aaagccaagg ccaatggtat cactatgtat gctgttgggg 2460
taggaaaagc cattgaggag gaactacaag agattgcctc tgagcccaca aacaagcatc 2520
tcttctatgc cgaagacttc agcacaatgg atgagataag tgaaaaactc aagaaaggca 2580
tctgtgaagc tctagaagac tccgatggaa gacaggactc tccagcaggg gaactgcca 2640
aaacgggtcca acagccaaca gaatctgagc cagtcaccat aaatatccaa gacctacttt 2700
cctgttctaa ttttgagtg caacacagat atctgtttga agaagacaat cttttacgg 2760
ctacacaaaa gctttcccat tcaacaaaac cttcaggaag ccctttggaa gaaaaacacg 2820
atcaatgcaa atgtgaaaac cttataatgt tccagaacct tgcaaacgaa gaagtaagaa 2880
aattaacaca gcgcttagaa gaaatgacac agagaatgga agcctggaa aatcgctga 2940
gatacagatg aagattagaa atcgcgacac atttgtagtc attgtatcac ggattacaat 3000
gaacgcagtg cagagcccca aagctcaggc tattgtttaa tcaataatgt tgtgaagtaa 3060
aacaatcagt actgagaaac ctggtttgcc acagaacaaa gacaagaagt atacactaac 3120
ttgtataaat ttatctagga aaaaaatcct tcagaattct aagatgaatt taccaggtga 3180
gaatgaataa gctatgcaag gtattttgtg atatactgtg gacacaactt gcttctgct 3240
catcctgcct tagtgtgcaa tctcatttga ctatacgata aagtttgcac agtcttactt 3300

```


225					230				235				240				
Met	Cys	Ser	Thr	Leu	Glu	His	Asn	Cys	Ala	His	Phe	Cys	Ile	Asn	Ile		
				245					250					255			
Pro	Gly	Ser	Tyr	Val	Cys	Arg	Cys	Lys	Gln	Gly	Tyr	Ile	Leu	Asn	Ser		
				260					265					270			
Asp	Gln	Thr	Thr	Cys	Arg	Ile	Gln	Asp	Leu	Cys	Ala	Met	Glu	Asp	His		
				275					280					285			
Asn	Cys	Glu	Gln	Leu	Cys	Val	Asn	Val	Pro	Gly	Ser	Phe	Val	Cys	Gln		
				290					295					300			
Cys	Tyr	Ser	Gly	Tyr	Ala	Leu	Ala	Glu	Asp	Gly	Lys	Arg	Cys	Val	Ala		
305					310					315					320		
Val	Asp	Tyr	Cys	Ala	Ser	Glu	Asn	His	Gly	Cys	Glu	His	Glu	Cys	Val		
				325					330					335			
Asn	Ala	Asp	Gly	Ser	Tyr	Leu	Cys	Gln	Cys	His	Glu	Gly	Phe	Ala	Leu		
				340					345					350			
Asn	Pro	Asp	Glu	Lys	Thr	Cys	Thr	Arg	Ile	Asn	Tyr	Cys	Ala	Leu	Asn		
				355					360					365			
Lys	Pro	Gly	Cys	Glu	His	Glu	Cys	Val	Asn	Met	Glu	Glu	Ser	Tyr	Tyr		
				370					375					380			
Cys	Arg	Cys	His	Arg	Gly	Tyr	Thr	Leu	Asp	Pro	Asn	Gly	Lys	Thr	Cys		
385					390					395					400		
Ser	Arg	Val	Asp	His	Cys	Ala	Gln	Gln	Asp	His	Gly	Cys	Glu	Gln	Leu		
				405					410					415			
Cys	Leu	Asn	Thr	Glu	Asp	Ser	Phe	Val	Cys	Gln	Cys	Ser	Glu	Gly	Phe		
				420					425					430			
Leu	Ile	Asn	Glu	Asp	Leu	Lys	Thr	Cys	Ser	Arg	Val	Asp	Tyr	Cys	Leu		
				435					440					445			
Leu	Ser	Asp	His	Gly	Cys	Glu	Tyr	Ser	Cys	Val	Asn	Met	Asp	Arg	Ser		
				450					455					460			
Phe	Ala	Cys	Gln	Cys	Pro	Glu	Gly	His	Val	Leu	Arg	Ser	Asp	Gly	Lys		
465					470					475					480		
Thr	Cys	Ala	Lys	Leu	Asp	Ser	Cys	Ala	Leu	Gly	Asp	His	Gly	Cys	Glu		
				485					490					495			
His	Ser	Cys	Val	Ser	Ser	Glu	Asp	Ser	Phe	Val	Cys	Gln	Cys	Phe	Glu		
				500					505					510			

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 37

gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag

45

<210> 38

<211> 1813

<212> DNA

<213> Homo sapiens

<400> 38

```

ggagccgccc tgggtgtcag cggctcggct cccgcgcacg ctccggccgt cgcgcagcct 60
cggcacctgc aggtccgtgc gtcccgcggc tggcgccccct gactccgtcc cggccagggg 120
gggccatgat ttccctcccg gggccccctg tgaccaactt gctgcggttt ttgttccctg 180
ggctgagtgc cctcgcgccc ccctcgcggg cccagctgca actgcacttg cccgccaaac 240
ggttgcaggg ggtggagggg ggggaagtgg tgcttcacg gtggtacacc ttgcacgggg 300
aggtgtcttc atcccagcca tgggaggtgc cctttgtgat gtggttcttc aaacagaaag 360
aaaaggagga tcaggtgttg tccatgccc tcccgaacc tgtccctgcg gctggagggt ctccaggaga 420
ccttgggtcta cccatgccc tcccgaacc tgtccctgcg gctggagggt ctccaggaga 480
aagactctgg cccctacagc tgctccgtga atgtgcaaga caaacaaggc aaatctaggg 540
gccacagcat caaaacctta gaactcaatg tactggttcc tccagctcct ccacctgcc 600
gtctccaggg tgtgccccat gtgggggcaa acgtgaccct gagctgccag tctccaagga 660
gtaagcccg tgtccaatac cagtgggatc ggcagcttcc atccttccag actttctttg 720
caccagcatt agatgtcatc cgtgggtctt taagcctcac caacctttcg tcttccatgg 780
ctggagtcta tgtctgcaag gccacaatg aggtgggcac tgcccaatgt aatgtgacgc 840
tggaagtgag cacagggcct ggagctgcag tggttgctgg agctgttgtg ggtaccctgg 900
ttggactggg gttgctggct gggctgggtc tcttgtacca ccgcccggggc aaggccctgg 960
aggagccagc caatgatata aaggaggatg ccattgctcc ccggaccctg ccctggccca 1020
agagctcaga cacaatctcc aagaatggga ccctttcttc tgtcacctcc gcacgagccc 1080
tccggccacc ccattggcct cccaggcctg gtgcattgac cccacgccc agtctctcca 1140
gccaggccct gccctacca agactgccc cgacagatgg ggcccacct caaccaatat 1200
ccccatccc tgggtggggt tcttctctg gcttgagccg catgggtgct gtgctgtga 1260
tgggtgctgc ccagagtcaa gctggctctc tggtatgat accccaccac tcattggcta 1320
aaggatttgg ggtctctcct tctataagg gtcacctcta gcacagaggc ctgagtcag 1380
ggaaagagtc aactcctga cccttagtac tctgccccca cctctcttta ctgtgggaaa 1440
accatctcag taagacctaa gtgtccagga gacagaagga gaagaggaag tggatctgga 1500
attgggagga gcctccacc accctgact cctccttatg aagccagctg ctgaaattag 1560
ctactacca agagtgagg gacagactt ccagtcactg agtctcccag gccccttga 1620
tctgtacccc acccctatct aacaccacc ttggctccca ctccagctcc ctgtattgat 1680
ataacctgtc aggtggctt gggttaggtt tactggggca gaggataggg aatctcttat 1740
taaaactaac atgaaatatg tggtgttttc atttgcaaat ttaaataaag atacataatg 1800
tttgtatgaa aaa 1813

```

<210> 39

<211> 390

<212> PRT

<213> Homo sapiens

<400> 39

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1					5					10					15				
Phe	Leu	Gly	Leu	Ser	Ala	Leu	Ala	Pro	Pro	Ser	Arg	Ala	Gln	Leu	Gln				
			20					25					30						
Leu	His	Leu	Pro	Ala	Asn	Arg	Leu	Gln	Ala	Val	Glu	Gly	Gly	Glu	Val				
			35					40					45						
Val	Leu	Pro	Ala	Trp	Tyr	Thr	Leu	His	Gly	Glu	Val	Ser	Ser	Ser	Gln				
			50					55					60						
Pro	Trp	Glu	Val	Pro	Phe	Val	Met	Trp	Phe	Phe	Lys	Gln	Lys	Glu	Lys				
			65					70					75						
Glu	Asp	Gln	Val	Leu	Ser	Tyr	Ile	Asn	Gly	Val	Thr	Thr	Ser	Lys	Pro				
				85					90					95					
Gly	Val	Ser	Leu	Val	Tyr	Ser	Met	Pro	Ser	Arg	Asn	Leu	Ser	Leu	Arg				
			100					105					110						
Leu	Glu	Gly	Leu	Gln	Glu	Lys	Asp	Ser	Gly	Pro	Tyr	Ser	Cys	Ser	Val				
			115					120					125						
Asn	Val	Gln	Asp	Lys	Gln	Gly	Lys	Ser	Arg	Gly	His	Ser	Ile	Lys	Thr				
			130					135					140						
Leu	Glu	Leu	Asn	Val	Leu	Val	Pro	Pro	Ala	Pro	Pro	Ser	Cys	Arg	Leu				
				150					155						160				
Gln	Gly	Val	Pro	His	Val	Gly	Ala	Asn	Val	Thr	Leu	Ser	Cys	Gln	Ser				
				165					170					175					
Pro	Arg	Ser	Lys	Pro	Ala	Val	Gln	Tyr	Gln	Trp	Asp	Arg	Gln	Leu	Pro				
			180					185					190						
Ser	Phe	Gln	Thr	Phe	Phe	Ala	Pro	Ala	Leu	Asp	Val	Ile	Arg	Gly	Ser				
			195					200					205						
Leu	Ser	Leu	Thr	Asn	Leu	Ser	Ser	Ser	Met	Ala	Gly	Val	Tyr	Val	Cys				
			210					215					220						
Lys	Ala	His	Asn	Glu	Val	Gly	Thr	Ala	Gln	Cys	Asn	Val	Thr	Leu	Glu				
			225					230					235						
Val	Ser	Thr	Gly	Pro	Gly	Ala	Ala	Val	Val	Ala	Gly	Ala	Val	Val	Gly				
				245					250					255					
Thr	Leu	Val	Gly	Leu	Gly	Leu	Leu	Ala	Gly	Leu	Val	Leu	Leu	Tyr	His				
			260					265					270						
Arg	Arg	Gly	Lys	Ala	Leu	Glu	Glu	Pro	Ala	Asn	Asp	Ile	Lys	Glu	Asp				
			275					280					285						

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 42
 ggccacagca tcaaaacctt agaactcaat gtactgggtc ctccagctcc 50

 <210> 43
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 43
 gtgtgacaca gcgtgggc 18

 <210> 44
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 44
 gaccggcagg cttctgcg 18

 <210> 45
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 45
 cagcagcttc agccaccagg agtgg 25

 <210> 46
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 46
 ctgagccgtg ggctgcagtc tcgc 24

 <210> 47

<211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 47
 ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc 45

<210> 48
 <211> 2822
 <212> DNA
 <213> Homo sapiens

<400> 48
 cgccaccact gcggccaccg ccaatgaaac gcctcccgt cctagtgggt ttttccactt 60
 tgttgaattg ttctataact caaaattgca ccaagacacc ttgtctccca aatgcaaaat 120
 gtgaaatacg caatggaatt gaagcctgct attgcaacat gggattttca ggaaatgggtg 180
 tcacaatttg tgaagatgat aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg 240
 ctaattgcac taacacagaa ggaagttatt attgtatgtg tgtacctggc ttcagatcca 300
 gcagtaacca agacagggtt atcactaatg atggaaccgt ctgtatagaa aatgtgaatg 360
 caaactgcca tttagataat gtctgtatag ctgcaaatat taataaaact ttaacaaaaa 420
 tcagatccat aaaagaacct gtggctttgc tacaagaagt ctatagaaat tctgtgacag 480
 atctttcacc aacagatata attacatata tagaaatatt agctgaatca tcttcattac 540
 taggttacaa gaacaacact atctcagcca aggacacct ttctaactca actcttactg 600
 aatttgtaaa aaccgtgaat aattttgttc aaagggatac atttgtagt tgggacaagt 660
 tatctgtgaa tcataggaga acacatctta caaaactcat gcacactgtt gaacaagcta 720
 ctttaaggat atcccagagc ttccaaaaga ccacagagtt tgatacaaat tcaacggata 780
 tagctctcaa agttttcttt tttgattcat ataacatgaa acatattcat cctcatatga 840
 atatggatgg agactacata aatatatttc caaagagaaa agctgcatat gattcaaatg 900
 gcaatgttgc agttgcattt ttatattata agagtattgg tcctttgctt tcatcatctg 960
 acaacttctt attgaaacct caaaattatg ataattctga agaggaggaa agagtcatat 1020
 cttcagtaat ttcagtctca atgagctcaa acccaccac attatatgaa cttgaaaaaa 1080
 taacatttac attaagtcac cgaaaggcca cagataggta taggagtcta tgtgcatttt 1140
 ggaattactc acctgatacc atgaatggca gctggctctc agagggctgt gagctgacat 1200
 actcaaatga gaccacaccc tcatgccgct gtaatcacct gacacatttt gcaattttga 1260
 tgtcctctgg tccttccatt ggtattaaag attataatat tcttacaagg atcactcaac 1320
 taggaataat tatttcactg atttgtcttg ccatatgcat ttttaccttc tggttcttca 1380
 gtgaaattca aagcaccagg acaacaattc acaaaaatct ttgctgtagc ctatttcttg 1440
 ctgaacttgt ttttcttggt gggatcaata caaatactaa taagctcttc tgttcaatca 1500
 ttgccggact gctacactac ttcttttttag ctgcttttgc atggatgtgc attgaaggca 1560
 tacatctcta tctcattgtt gtgggtgtca tctacaacaa gggatttttg cacaagaatt 1620
 tttatatctt tggctatcta agcccagccg tggtagttgg attttcggca gcactaggat 1680
 acagatatta tggcacaacc aaagtatgtt ggcttagcac cgaaaacaac tttatttgga 1740
 gttttatagg accagcatgc ctaatcattc ttgttaatct cttggctttt ggagtcacat 1800
 tatacaaagt ttttcgtcac actgcagggt tgaaaccaga agttagttgc tttgagaaca 1860
 taaggtcttg tgcaagagga gccctcgctc ttctgttctt tctcggcacc acctggatct 1920
 ttggggttct ccatgttgtg cagcatcag tggttacagc ttacctcttc acagtcagca 1980
 atgctttcca ggggatgttc atttttttat tctgtgtgtg tttatctaga aagattcaag 2040
 aagaatatta cagattgttc aaaaatgtcc cctgttgttt tggatgttta aggtaaacat 2100
 agagaatggg ggataattac aactgcacaa aaataaaaat tccaagctgt ggatgaccaa 2160

```
<210> 49
<211> 690
<212> PRT
<213> Homo sapiens
```

Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys
1 5 10 15

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
35 40 45

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
50 55 60

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
65 70 75 80

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
85 90 95

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
100 105 110

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
115 120 125

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
130 135 140

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
145 150 155 160

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
165 170 175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

180						185						190				
Glu	Phe	Val	Lys	Thr	Val	Asn	Asn	Phe	Val	Gln	Arg	Asp	Thr	Phe	Val	
		195				200						205				
Val	Trp	Asp	Lys	Leu	Ser	Val	Asn	His	Arg	Arg	Thr	His	Leu	Thr	Lys	
		210				215				220						
Leu	Met	His	Thr	Val	Glu	Gln	Ala	Thr	Leu	Arg	Ile	Ser	Gln	Ser	Phe	
		225			230					235						240
Gln	Lys	Thr	Thr	Glu	Phe	Asp	Thr	Asn	Ser	Thr	Asp	Ile	Ala	Leu	Lys	
				245					250				255			
Val	Phe	Phe	Phe	Asp	Ser	Tyr	Asn	Met	Lys	His	Ile	His	Pro	His	Met	
		260						265				270				
Asn	Met	Asp	Gly	Asp	Tyr	Ile	Asn	Ile	Phe	Pro	Lys	Arg	Lys	Ala	Ala	
		275					280				285					
Tyr	Asp	Ser	Asn	Gly	Asn	Val	Ala	Val	Ala	Phe	Leu	Tyr	Tyr	Lys	Ser	
		290			295						300					
Ile	Gly	Pro	Leu	Leu	Ser	Ser	Ser	Asp	Asn	Phe	Leu	Leu	Lys	Pro	Gln	
		305			310					315				320		
Asn	Tyr	Asp	Asn	Ser	Glu	Glu	Glu	Glu	Arg	Val	Ile	Ser	Ser	Val	Ile	
				325					330				335			
Ser	Val	Ser	Met	Ser	Ser	Asn	Pro	Pro	Thr	Leu	Tyr	Glu	Leu	Glu	Lys	
		340						345				350				
Ile	Thr	Phe	Thr	Leu	Ser	His	Arg	Lys	Val	Thr	Asp	Arg	Tyr	Arg	Ser	
		355				360						365				
Leu	Cys	Ala	Phe	Trp	Asn	Tyr	Ser	Pro	Asp	Thr	Met	Asn	Gly	Ser	Trp	
		370			375						380					
Ser	Ser	Glu	Gly	Cys	Glu	Leu	Thr	Tyr	Ser	Asn	Glu	Thr	His	Thr	Ser	
		385			390					395				400		
Cys	Arg	Cys	Asn	His	Leu	Thr	His	Phe	Ala	Ile	Leu	Met	Ser	Ser	Gly	
				405					410				415			
Pro	Ser	Ile	Gly	Ile	Lys	Asp	Tyr	Asn	Ile	Leu	Thr	Arg	Ile	Thr	Gln	
		420						425				430				
Leu	Gly	Ile	Ile	Ile	Ser	Leu	Ile	Cys	Leu	Ala	Ile	Cys	Ile	Phe	Thr	
		435				440						445				
Phe	Trp	Phe	Phe	Ser	Glu	Ile	Gln	Ser	Thr	Arg	Thr	Thr	Ile	His	Lys	
		450				455				460						

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly
 465 470 475 480

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu
 485 490 495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly
 500 505 510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe
 515 520 525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val
 530 535 540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
 545 550 555 560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
 565 570 575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile
 580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
 595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
 610 615 620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His
 625 630 635 640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
 645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
 660 665 670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys
 675 680 685

Leu Arg
 690

<210> 50

<211> 589

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (61)

PEPTIDE SEQUENCE

<223> a, t, c or g

<400> 50

```

tggaacata tcctccctca tatgaatatg gatggagact acataaatat atttccaaag 60
ngaaaagccg gcatatggat tcaaattggca atgttgagc tgcattttta tattataaga 120
gtattgggtcc ctttgctttc atcatctgac aacttcttat tgaaacctca aaattatgat 180
aattctgaag aggaggaaag agtcatatct tcagtaattt cagtctcaat gagctcaaac 240
ccaccacat tatatgaact tgaaaaaata acatttacat taagtcacgc aaaggtcaca 300
gatagggtata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360
tggctcttcag agggctgtga gctgacatac tcaaattgaga cccacacctc atgccgctgt 420
aatcacctga cacattttgc aattttgatg tctcttggtc cttccattgg tattaaagat 480
tataatattc ttacaaggat cactcaacta ggaataatta tttcactgat ttgtcttgcc 540
atatgcattt ttaccttctg gttcttcagt gaaattcaaa gcaccagga 589

```

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 51

ggtaatgagc tccattacag 20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 52

ggagtagaaa gcgcatgg 18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag 22

<210> 54

<211> 18

<212> DNA

Sequence

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 55

ggatctcctg agtcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 56

cctagttgag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 57

atgagacca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

gctcccagcc aagaacctcg gggccgctgc gcggtgggga ggagttcccc gaaacccggc 60
cgctaagcga ggcctcctcc tcccgcagat ccgaacggcc tgggcgggggt caccgcggct 120

Sequence

gggacaagaa gccgcgcgct gcctgcccgg gcccggggag ggggctgggg ctggggccgg 180
 aggcgggggtg tgagtgggtg tgtgcggggg gcggaggctt gatgcaatcc cgataagaaa 240
 tgctcgggtg tcttgggcac ctaccctggg ggcccgtaag gcgctactat ataaggctgc 300
 cggcccgagag ccgcccgcgc gtcagagcag ggcgctgcg tccaggatct agggccacga 360
 ccatacccaac ccggcactca cagccccgca gcgcaccccg gtccgcgccc agcctcccgc 420
 acccccactcg ccggagctgc gccgagagcc ccaggagggt gccatgcgga gcgggtgtgt 480
 ggtgggtccac gtatggatcc tggccggcct ctggctggcc gtggccgggc gccccctcgc 540
 cttctcggac gcggggcccc acgtgcaacta cggctggggc gaccccatcc gcctgcggca 600
 cctgtacacc tccggcccc acgggctctc cagctgcttc ctgcgcatcc gtgccgacgg 660
 cgtcgtggac tgcgcgcggg gccagagcgc gcacagttt ctggagatca aggcagtcgc 720
 tctgcggacc gtggccatca agggcgtgca cagcgtgcgg tacctctgca tgggcgcga 780
 cggcaagatg caggggctgc ttcagtactc ggaggaagac tgtgctttcg aggaggagat 840
 ccgcccagat ggctacaatg tgtaccgatc cgagaagcac cgcctcccgg tctccctgag 900
 cagtgccaaa cagcggcagc tgtacaagaa cagaggcttt cttccactct ctcatcttct 960
 gcccatgctg cccatgggtc cagaggagcc tgaggacctc agggggccact tggaatctga 1020
 catgttctct tcgcccctgg agaccgacag catggaccca tttgggcttg tcaccggact 1080
 ggaggccgtg aggagtccca gctttgagaa gtaactgaga ccatgcccgg gcctcttcac 1140
 tgctgccagg ggctgtggtg cctgcagcgt gggggacgtg cttctacaag aacagtcctg 1200
 agtccacgtt ctgtttagct ttaggaagaa acatctagaa gttgtacata ttcagagttt 1260
 tccattggca gtgccagttt ctagccaata gacttgtctg atcataacat tgtaagcctg 1320
 tagcttgccc agctgctgcc tgggccccca ttctgctccc tcgaggttgc tggacaagct 1380
 gctgcactgt ctcagttctg cttgaatacc tccatcgatg gggaaactcac ttcctttgga 1440
 aaaattctta tgtcaagctg aaattctcta atttttctc atcacttccc caggagcagc 1500
 cagaagacag gcagtagttt taatttcagg aacagggtgat ccactctgta aaacagcagg 1560
 taaatttcac tcaaccccat gtgggaattg atctatatct ctacttccag ggaccatttg 1620
 cccttcccaa atccctccag gccagaactg actggagcag gcatggccca ccaggcttca 1680
 ggagtggggg aagcctggag ccccaactca gccctgggac aacttgagaa tccccctga 1740
 ggccagttct gtcattggat ctgtcctgag aataacttgc tgtcccgggtg tcacctgctt 1800
 ccatttccca gccaccagc cctctgcccc cctcacatgc ctccccatgg attggggcct 1860
 cccaggcccc ccaccttatg tcaacctgca cttcttggtc aaaaatcagg aaaagaaaag 1920
 atttgaagac cccaagtctt gtcaataact tgctgtgtgg aagcagcggg ggaagacctt 1980
 gaaccctttc ccagcactt ggttttccaa catgatattt atgagtaatt tattttgata 2040
 tgtacatctc ttattttctt acattattta tgccccaaa ttatatattt gtatgtaagt 2100
 gaggtttgtt ttgtatatta aaatggagtt tgtttgt 2137

<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

Met	Arg	Ser	Gly	Cys	Val	Val	Val	His	Val	Trp	Ile	Leu	Ala	Gly	Leu
1				5					10					15	

Trp	Leu	Ala	Val	Ala	Gly	Arg	Pro	Leu	Ala	Phe	Ser	Asp	Ala	Gly	Pro
			20					25						30	

His	Val	His	Tyr	Gly	Trp	Gly	Asp	Pro	Ile	Arg	Leu	Arg	His	Leu	Tyr
			35				40					45			

Thr	Ser	Gly	Pro	His	Gly	Leu	Ser	Ser	Cys	Phe	Leu	Arg	Ile	Arg	Ala
			50			55						60			

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
 65 70 75 80
 Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
 85 90 95
 Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
 100 105 110
 Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro
 115 120 125
 Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
 130 135 140
 Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
 145 150 155 160
 Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
 165 170 175
 Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
 180 185 190
 Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
 195 200 205
 Val Arg Ser Pro Ser Phe Glu Lys
 210 215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 60

atccgcccag atggctacaa tgtgta

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 61

gcctcccggc ctcctgagc agtgccaaac agcggcagtg ta

42

F
O
R
M
A
T
E
D
S
E
Q
U
E
N
C
E
S

Lys	Asp	Gln	Gln	Val	Val	Thr	Ala	Val	Glu	Tyr	Gln	Glu	Ala	Ile	Leu
35						40						45			
Ala	Cys	Lys	Thr	Pro	Lys	Lys	Thr	Val	Ser	Ser	Arg	Leu	Glu	Trp	Lys
50						55				60					
Lys	Leu	Gly	Arg	Ser	Val	Ser	Phe	Val	Tyr	Tyr	Gln	Gln	Thr	Leu	Gln
65				70						75				80	
Gly	Asp	Phe	Lys	Asn	Arg	Ala	Glu	Met	Ile	Asp	Phe	Asn	Ile	Arg	Ile
				85						90				95	
Lys	Asn	Val	Thr	Arg	Ser	Asp	Ala	Gly	Lys	Tyr	Arg	Cys	Glu	Val	Ser
		100						105				110			
Ala	Pro	Ser	Glu	Gln	Gly	Gln	Asn	Leu	Glu	Glu	Asp	Thr	Val	Thr	Leu
		115				120						125			
Glu	Val	Leu	Val	Ala	Pro	Ala	Val	Pro	Ser	Cys	Glu	Val	Pro	Ser	Ser
130						135				140					
Ala	Leu	Ser	Gly	Thr	Val	Val	Glu	Leu	Arg	Cys	Gln	Asp	Lys	Glu	Gly
145				150						155				160	
Asn	Pro	Ala	Pro	Glu	Tyr	Thr	Trp	Phe	Lys	Asp	Gly	Ile	Arg	Leu	Leu
				165						170				175	
Glu	Asn	Pro	Arg	Leu	Gly	Ser	Gln	Ser	Thr	Asn	Ser	Ser	Tyr	Thr	Met
		180						185				190			
Asn	Thr	Lys	Thr	Gly	Thr	Leu	Gln	Phe	Asn	Thr	Val	Ser	Lys	Leu	Asp
195						200						205			
Thr	Gly	Glu	Tyr	Ser	Cys	Glu	Ala	Arg	Asn	Ser	Val	Gly	Tyr	Arg	Arg
210						215				220					
Cys	Pro	Gly	Lys	Arg	Met	Gln	Val	Asp	Asp	Leu	Asn	Ile	Ser	Gly	Ile
225				230						235				240	
Ile	Ala	Ala	Val	Val	Val	Val	Ala	Leu	Val	Ile	Ser	Val	Cys	Gly	Leu
				245				250						255	
Gly	Val	Cys	Tyr	Ala	Gln	Arg	Lys	Gly	Tyr	Phe	Ser	Lys	Glu	Thr	Ser
		260						265				270			
Phe	Gln	Lys	Ser	Asn	Ser	Ser	Ser	Lys	Ala	Thr	Thr	Met	Ser	Glu	Asn
275						280						285			
Val	Gln	Trp	Leu	Thr	Pro	Val	Ile	Pro	Ala	Leu	Trp	Lys	Ala	Ala	Ala
290						295				300					
Gly	Gly	Ser	Arg	Gly	Gln	Glu	Phe								

310

<211> 22

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 65

atcattgtga agttagtgcc cc

22

<210> 66

<211> 23

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 66

acctgcgata tccaacagaa ttg

23

<210> 67

<211> 48

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 67

qgaagaggat acaqtcactc tggaaqtatt agtggctcca qcaqttcc

48

<210> 68

<211> 2639

<212> DNA

<213> Homo sapiens

<400> 68

gacatcggag	gtgggctagc	actgaaactg	cttttcaaga	cgaggaagag	gaggagaaaag	60
agaaagaaga	ggaagatgtt	gggcaacatt	tattttaacat	gctccacagc	cgggaccttg	120
gcatcatgct	gctattcctg	caaatactga	agaagcatgg	gattttaaata	ttttacttct	180
aaataaatga	attactcaat	ctcctatgac	catctataca	tactccacct	tcaaaaagta	240
catcaatatt	atatcattaa	ggaaatagta	accttctctt	ctccaatatg	catgacattt	300
ttggacaatg	caattgtggc	actggcactt	atttcagtga	agaaaaaactt	tgtggttcta	360
tggcattcat	catttgacaa	atgcaagcat	cttccttata	aatcagctcc	tattgaactt	420
actagcactg	actgtggaat	ccttaagggc	ccattacatt	tctgaagaag	aaagctaaga	480
tgaagqacat	gccactccga	attcatgtgc	tacttggcct	agctatcact	acactagtac	540

```

aagctgtaga taaaaaagtg gattgtccac gggtatgtac gtgtgaaatc aggccttggg 600
ttacaccag atccatttat atggaagcat ctacagtgga ttgtaatgat ttaggtcttt 660
taactttccc agccagattg ccagctaaca cacagattct tctcctacag actaacaata 720
ttgcaaaaat tgaatactcc acagactttc cagtaaacct tactggcctg gatttatctc 780
aaaacaattt atcttcagtc accaatatta atgtaaaaaa gatgcctcag ctcccttctg 840
tgtacctaga ggaaaacaaa cttactgaac tgcctgaaaa atgtctgtcc gaactgagca 900
acttacaaga actctatatt aatcacaaact tgctttctac aatttcacct ggagccttta 960
ttggcctaca taatcttctt cgacttcac tcaattcaaa tagattgcag atgatcaaca 1020
gtaagtgggt tgatgctctt ccaaacttag agattctgat gattggggaa aatccaatta 1080
tcagaatcaa agacatgaac tttaagcctc ttatcaatct tgcagcctg gttatagctg 1140
gtataaacct cacagaaata ccagataacg ccttgggttg actggaaaac ttagaaagca 1200
tctcttttta cgataacagg cttattaaag taccctatgt tgccttcaa aaagttgtaa 1260
atctcaaatt tttggatcta aataaaaaat ctattaatag aatacgaagg ggtgatttta 1320
gcaatatgct acacttaaaa gagttgggga taaataatat gcctgagctg atttccatcg 1380
atagtcttgc tgtggataac ctgccagatt taagaaaaat agaagctact aacaacctta 1440
gattgtctta cattcacccc aatgcatttt tcagactccc caagctggaa tcaactcatgc 1500
tgaacagcaa tgctctcagt gccctgtacc atggtaccat tgagtctctg ccaaacctca 1560
aggaaatcag catacacagt aaccccatca ggtgtgactg tgcacccgt tggatgaaca 1620
tgaacaaaac caacattcga ttcatggagc cagattcact gttttgcgtg gaccacctg 1680
aattccaagg tcagaatgtt cggcaagtgc atttcaggga catgatggaa atttgtctcc 1740
ctcttatagc tcttgagagc ttctcttcta atctaaatgt agaagctggg agctatgttt 1800
cctttcactg tagagctact gcagaaccac agcctgaaat ctactggata acaccttctg 1860
gtcaaaaact cttgcctaact accctgacag acaagttcta tgtccattct gagggaacac 1920
tagatataaa tggcgtaact cccaaagaag ggggtttata tacttgtata gcaactaacc 1980
tagttggcgc tgacttgaag tctgttatga tcaaagtgga tggatctttt ccacaagata 2040
acaatggctc tttgaatatt aaaataagag atattcaggc caattcagtt ttggtgtcct 2100
ggaaagcaag ttctaaaatt ctcaaactta gtgttaaag gacagccttt gtcaagactg 2160
aaaatttctc tgctgcgcaa agtgctcgaa taccatctga tgtcaaggta tataatctta 2220
ctcatctgaa tccatcaact gagtataaaa tttgtattga tattcccacc atctatcaga 2280
aaaacagaaa aaaatgtgta aatgtcacca ccaaagggtt gcaccctgat caaaaagagt 2340
atgaaaagaa taataccaca acacttatgg cctgtcttgg aggccttctg gggattattg 2400
gtgtgatatg tcttatcagc tgccctctctc cagaaatgaa ctgtgatggg ggacacagct 2460
atgtgaggaa ttacttacag aaaccaacct ttgcattagg tgagctttat cctcctctga 2520
taaattctctg ggaagcagga aaagaaaaaa gtacatcact gaaagtaaaa gcaactgtta 2580
taggtttacc aacaaatatg tcttaaaaac caccaaggaa acctactcca aaaatgaac 2639

```

<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile
1 5 10 15

Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu
20 25 30

Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met
35 40 45

Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
50 55 60

340							345					350				
Thr	Ile	Glu	Ser	Leu	Pro	Asn	Leu	Lys	Glu	Ile	Ser	Ile	His	Ser	Asn	
		355				360						365				
Pro	Ile	Arg	Cys	Asp	Cys	Val	Ile	Arg	Trp	Met	Asn	Met	Asn	Lys	Thr	
		370				375						380				
Asn	Ile	Arg	Phe	Met	Glu	Pro	Asp	Ser	Leu	Phe	Cys	Val	Asp	Pro	Pro	
				390						395				400		
Glu	Phe	Gln	Gly	Gln	Asn	Val	Arg	Gln	Val	His	Phe	Arg	Asp	Met	Met	
				405				410						415		
Glu	Ile	Cys	Leu	Pro	Leu	Ile	Ala	Pro	Glu	Ser	Phe	Pro	Ser	Asn	Leu	
		420						425				430				
Asn	Val	Glu	Ala	Gly	Ser	Tyr	Val	Ser	Phe	His	Cys	Arg	Ala	Thr	Ala	
		435				440						445				
Glu	Pro	Gln	Pro	Glu	Ile	Tyr	Trp	Ile	Thr	Pro	Ser	Gly	Gln	Lys	Leu	
		450				455						460				
Leu	Pro	Asn	Thr	Leu	Thr	Asp	Lys	Phe	Tyr	Val	His	Ser	Glu	Gly	Thr	
				470						475				480		
Leu	Asp	Ile	Asn	Gly	Val	Thr	Pro	Lys	Glu	Gly	Gly	Leu	Tyr	Thr	Cys	
				485				490						495		
Ile	Ala	Thr	Asn	Leu	Val	Gly	Ala	Asp	Leu	Lys	Ser	Val	Met	Ile	Lys	
		500						505				510				
Val	Asp	Gly	Ser	Phe	Pro	Gln	Asp	Asn	Asn	Gly	Ser	Leu	Asn	Ile	Lys	
		515				520						525				
Ile	Arg	Asp	Ile	Gln	Ala	Asn	Ser	Val	Leu	Val	Ser	Trp	Lys	Ala	Ser	
		530				535						540				
Ser	Lys	Ile	Leu	Lys	Ser	Ser	Val	Lys	Trp	Thr	Ala	Phe	Val	Lys	Thr	
		545		550						555				560		
Glu	Asn	Ser	His	Ala	Ala	Gln	Ser	Ala	Arg	Ile	Pro	Ser	Asp	Val	Lys	
				565				570						575		
Val	Tyr	Asn	Leu	Thr	His	Leu	Asn	Pro	Ser	Thr	Glu	Tyr	Lys	Ile	Cys	
		580				585						590				
Ile	Asp	Ile	Pro	Thr	Ile	Tyr	Gln	Lys	Asn	Arg	Lys	Lys	Cys	Val	Asn	
		595				600						605				
Val	Thr	Thr	Lys	Gly	Leu	His	Pro	Asp	Gln	Lys	Glu	Tyr	Glu	Lys	Asn	
		610				615				620						

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro
690 695 700

Thr Asn Met Ser
705

<210> 70

<211> 1305

<212> DNA

<213> Homo sapiens

<400> 70

```

gcccgaggact ggcgcaaggt gcccaagcaa ggaaagaaat aatgaagaga cacatgtgtt 60
agctgcagcc ttttgaaca cgcaagaagg aaatcaatag tgtggacagg gctggaacct 120
ttaccacgct tgttgagta gatgaggaat gggctcgtga ttatgctgac attccagcat 180
gaatctggta gacctgtggt taaccctgtc cctctccatg tgtctcctcc tacaaagttt 240
tgttcttatg atactgtgct ttcattctgc cagtatgtgt cccaagggct gtctttgttc 300
ttcctctggg ggtttaaatg tcacctgtag caatgcaaat ctcaaggaaa tacctagaga 360
tcttctctct gaaacagctc tactgtatct ggactccaat cagatcacat ctattcccaa 420
tgaaatTTTT aaggacctcc atcaactgag agttctcaac ctgtccaaaa atggcattga 480
gtttatcgat gagcatgcct tcaaaggagt agctgaaacc ttgcagactc tggacttgtc 540
cgacaatcgg attcaaagtg tgcacaaaaa tgccttcaat aacctgaagg ccagggccag 600
aattgccaac aaccctggc actgcgactg tactctacag caagttctga ggagcatggc 660
gtccaatcat gagacagccc acaacgtgat ctgtaaaacg tccgtgttgg atgaacatgc 720
tggcagacca ttctcaatg ctgccaacga cgctgacctt tgtaacctcc ctaaaaaaac 780
taccgattat gccatgctgg tcacctggtt tggctgggtc actatgggtg tctcatatgt 840
ggtatattat gtgaggcaaa atcaggagga tgcccgga cactcgaat acttgaaatc 900
cctgccaaagc aggcagaaga aagcagatga acctgatgat attagcactg tggatatagt 960
tccaaactga ctgtcattga gaaagaaaga aagtagtttg cgattgcagt agaaataagt 1020
ggtttacttc tcccatccat tgtaaacatt tgaaactttg tatttcagtt ttttttgaat 1080
tatgccactg ctgaactttt aacaaacact acaacataaa taatttgagt ttaggtgatc 1140
cacccttaa ttgtacccc gatggtatat ttctgagtaa gctactatct gaacattagt 1200
tagatccatc tcactattta ataatgaaat ttattttttt aattttaaaag caaataaaaag 1260
cttaactttg aacctaggga aaaaaaaaaa aaaaaaaaaa aaaca 1305

```

<210> 71

<211> 259

<212> PRT

<213> Homo sapiens

<400> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu
 1 5 10 15
 Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser
 20 25 30
 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val
 35 40 45
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro
 50 55 60
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro
 65 70 75 80
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser
 85 90 95
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala
 100 105 110
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val
 115 120 125
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn
 130 135 140
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met
 145 150 155 160
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val
 165 170 175
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala
 180 185 190
 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val
 195 200 205
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr
 210 215 220
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys
 225 230 235 240
 Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser
 245 250 255
 Thr Val Val

<210> 72

<211> 2290

<212> DNA
 <213> Homo sapiens

<400> 72

```

accgagccga gcggaaccgaa ggcgcgcccc agatgcaggt gagcaagagg atgctggcgg 60
ggggcgtag gagcatgccc agccccctcc tggcctgctg gcagcccatc ctctgctgg 120
tgctgggctc agtgtgtca ggcctggcca cgggctgccc gccccgctgc gaggctccg 180
cccaggaccg cgctgtgctg tgccaccgca agtgctttgt ggcagtcccc gaggccatcc 240
ccaccgagac gcgcctgctg gacctaggca agaaccgcat caaaacgctc aaccaggacg 300
agttcgccag cttccgcac ctggaggagc tggagctcaa cgagaacatc gtgagcgccg 360
tggagcccg cgcttcaac aacctcttca acctccgac gctgggtctc cgcagcaacc 420
gcctgaagct catcccgta ggcgtcttca ctggcctcag caacctgacc aagcaggaca 480
tcagcgagaa caagatcgtt atcctactgg actacatgtt tcaggacctg tacaacctca 540
agtcactgga ggttggcgac aatgacctcg tctacatctc tcaccgcgcc ttcagcggcc 600
tcaacagcct ggagcagctg acgctggaga aatgcaacct gacctccatc cccaccgagg 660
cgctgtccca cctgcacggc ctcatcgtcc tgaggctccg gcacctcaac atcaatgcca 720
tccgggacta ctcttcaag aggctgtacc gactcaaggt cttggagatc tccactggc 780
cctacttgga caccatgaca cccaactgcc tctacggcct caacctgacg tccctgtcca 840
tcacacactg caatctgacc gctgtgacct acctggcgt ccgccacctg gtctatctcc 900
gcttctctaa cctctctac aaccccatca gcaccattga gggctccatg ttgcatgagc 960
tgctccggct gcaggagatc cagctggtgg gcgggcagct ggcctggtg gagecctatg 1020
ccttccgcgg cctcaactac ctgcgcgtgc tcaatgtctc tggcaaccag ctgaccacac 1080
tggaggaatc agtcttccac tcgggtggga acctggagac actcatctg gactccaacc 1140
cgctggcctg cgactgtcgg ctctgtggg tgttccggcg ccgctggcgg ctcaacttca 1200
accggcagca gcccacgtgc gccacgccc agtttgtcca gggcaaggag ttcaaggact 1260
tccctgatgt gctactgcc aactacttca cctgcgcgcg cgcccgcatc cgggaccgca 1320
aggcccagca ggtgtttgtg gacgagggcc acacggtgca gtttgtgtgc cgggccgatg 1380
gcgacccgcc gcccgccatc ctctggctct caccgcgaaa gcacctggtc tcagccaaga 1440
gcaatgggcg gctcacagtc ttccctgatg gcacgctgga ggtgcgctac gccagggtac 1500
aggacaacgg cacgtacctg tgcctgcgg ccaacgcggg cggcaacgac tccatgcccg 1560
cccacctgca tgtgcgcagc tactcgccc actggcccca tcagcccaac aagaccttcg 1620
ctttcatctc caaccagccg ggcgagggag aggcccaacag caccgcgcgc actgtgcctt 1680
tccccttcga catcaagacc ctcatcatcg ccaccaccat gggttccatc tcttctctgg 1740
gcgtcgtcct cttctgcctg gtgtgtgtgt ttctctggag cgggggcaag ggcaacacaa 1800
agcacaacat cgagatcgag tatgtgcccc gaaagtcgga cgcaggcatc agctccgcgc 1860
acgcgccccg caagttcaac atgaagatga tatgaggccg gggcgggggg cagggacccc 1920
cgggcggcgg ggcaggggaa ggggcctggt cgcacactgc tcaactctca gtcttccca 1980
ctcctcctc acccttctac acacgttctc tttctcctc ccgcctccgt cccctgctgc 2040
ccccgcag ccctcaccac ctgcctcct tctaccagga cctcagaagc ccagacctgg 2100
ggacccacc tacacagggg cattgacaga ctggagttga aagccgacga accgacacgc 2160
ggcagagtca ataattcaat aaaaaagtta cgaactttct ctgtaacttg ggtttcaata 2220
attatggatt tttatgaaaa cttgaaataa taaaaagaga aaaaaactaa aaaaaaaaaa 2280
aaaaaaaaa 2290

```

<210> 73
 <211> 620
 <212> PRT
 <213> Homo sapiens

<400> 73

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro
 1 5 10 15

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly
 20 25 30
 Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys
 35 40 45
 Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala
 50 55 60
 Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys
 65 70 75 80
 Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His
 85 90 95
 Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro
 100 105 110
 Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser
 115 120 125
 Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn
 130 135 140
 Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp
 145 150 155 160
 Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp
 165 170 175
 Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser
 180 185 190
 Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr
 195 200 205
 Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His
 210 215 220
 Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg
 225 230 235 240
 Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr
 245 250 255
 Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His
 260 265 270
 Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr
 275 280 285
 Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly
 290 295 300

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0


```
<210> 74
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
```

```
<210> 75
<211> 23
<212> DNA
<213> Artificial Sequence
```

```
<400> 75
ataccagcta taaccaggct gcg                                     23
```

```
<210> 76
<211> 52
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

```
<400> 76
caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg 50
qq 52
```

```
<210> 77
<211> 22
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
```


<211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 82
 gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga 50

<210> 83
 <211> 1685
 <212> DNA
 <213> Homo sapiens

<400> 83
 cccacgcgtc cgcacctcgg ccccgggctc cgaagcggct cggggggcgcc ctttcgggtca 60
 acatcgtagt ccacccccctc cccatcccca gcccccgggg attcaggctc gccagcgccc 120
 agccagggag ccggccggga agcgcgatgg gggccccagc cgcctcgctc ctgctcctgc 180
 tctgtctgtt cgcttctgtc tgggcgccc gcgggggcaa cctctcccag gacgacagcc 240
 agccctggac atctgatgaa acagtgggtg ctggtggcac cgtgggtgctc aagtgccaaag 300
 tgaaagatca cgaggactca tccctgcaat ggtctaacc tgctcagcag actctctact 360
 ttggggagaa gagagccctt cgagataatc gaattcagct ggttacctct acgccccacg 420
 agctcagcat cagcatcagc aatgtggccc tggcagacga gggcgagtac acctgctcaa 480
 tcttcactat gcctgtgcga actgccaaagt cctcgtcac tgtgctagga attccacaga 540
 agcccatcat cactggttat aaatcttcat tacgggaaaa agacacagcc accctaaact 600
 gtcagtcttc tgggagcaag cctgcagccc ggctcacctg gagaaagggg gaccaagaac 660
 tccacggaga accaaccgcg atacaggaag atcccaatgg taaaaccttc actgtcagca 720
 gctcgggtgac attccagggt acccgggagg atgatggggc gagcatcgtg tgcctctgtg 780
 accatgaatc tctaaaggga gctgacagat ccacctctca acgcattgaa gttttatata 840
 caccaactgc gatgattagg ccagaccctc cccatcctcg tgaggggccag aagctgttgc 900
 tacactgtga gggtcgcggc aatccagtc cccagcagta cctatgggag aaggagggca 960
 gtgtgccacc cctgaagatg acccaggaga gtgccctgat ctccctttc ctcaacaaga 1020
 gtgacagtgg cacctacggc tgcacagcca ccagcaacat gggcagctac aaggcctact 1080
 acacctcaa tgtaaatgac cccagtcagg tgcctcctc ctccagcacc taccacgcca 1140
 tcatcggtgg gatcgtggct ttcattgtct tccctgctgt catcatgctc atcttccttg 1200
 gccactactt gatccggcac aaaggaaact acctgacaca tgaggcaaaa ggctccgacg 1260
 atgctccaga cgcggacacg gccatcatca atgcagaagg cgggcagtcg ggaggggacg 1320
 acaagaagga atatttcac tagaggcgcc tgcccacttc ctgcgcccc cagggggcct 1380
 gtggggactg ctggggcgtt caccaaccgc gaattgtaca gagcaaccgc agggccgccc 1440
 ctcccgttgc ctcccagcc caccacccc cctgtacaga atgtctgctt tgggtgcggg 1500
 tttgtactcg gtttggaatg gggagggagg agggcggggg gaggggaggg ttgccctcag 1560
 ccctttccgt ggcttctctg catttggggt attattattt ttgtaacaat cccaaatcaa 1620
 atctgtctcc aggctggaga ggcaggagcc ctgggggtgag aaaagcaaaa aacaaacaaa 1680
 aaaca 1685

<210> 84
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 84

Met 1	Gly	Ala	Pro	Ala	Ala	Ser	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Phe	Ala
				5				10						15	
Cys	Cys	Trp	Ala	Pro	Gly	Gly	Ala	Asn	Leu	Ser	Gln	Asp	Asp	Ser	Gln
			20					25					30		
Pro	Trp	Thr	Ser	Asp	Glu	Thr	Val	Val	Ala	Gly	Gly	Thr	Val	Val	Leu
			35				40					45			
Lys	Cys	Gln	Val	Lys	Asp	His	Glu	Asp	Ser	Ser	Leu	Gln	Trp	Ser	Asn
		50				55					60				
Pro	Ala	Gln	Gln	Thr	Leu	Tyr	Phe	Gly	Glu	Lys	Arg	Ala	Leu	Arg	Asp
65					70					75					80
Asn	Arg	Ile	Gln	Leu	Val	Thr	Ser	Thr	Pro	His	Glu	Leu	Ser	Ile	Ser
				85					90					95	
Ile	Ser	Asn	Val	Ala	Leu	Ala	Asp	Glu	Gly	Glu	Tyr	Thr	Cys	Ser	Ile
			100					105					110		
Phe	Thr	Met	Pro	Val	Arg	Thr	Ala	Lys	Ser	Leu	Val	Thr	Val	Leu	Gly
		115					120					125			
Ile	Pro	Gln	Lys	Pro	Ile	Ile	Thr	Gly	Tyr	Lys	Ser	Ser	Leu	Arg	Glu
		130				135					140				
Lys	Asp	Thr	Ala	Thr	Leu	Asn	Cys	Gln	Ser	Ser	Gly	Ser	Lys	Pro	Ala
145					150					155					160
Ala	Arg	Leu	Thr	Trp	Arg	Lys	Gly	Asp	Gln	Glu	Leu	His	Gly	Glu	Pro
				165					170					175	
Thr	Arg	Ile	Gln	Glu	Asp	Pro	Asn	Gly	Lys	Thr	Phe	Thr	Val	Ser	Ser
			180					185					190		
Ser	Val	Thr	Phe	Gln	Val	Thr	Arg	Glu	Asp	Asp	Gly	Ala	Ser	Ile	Val
		195					200					205			
Cys	Ser	Val	Asn	His	Glu	Ser	Leu	Lys	Gly	Ala	Asp	Arg	Ser	Thr	Ser
		210				215					220				
Gln	Arg	Ile	Glu	Val	Leu	Tyr	Thr	Pro	Thr	Ala	Met	Ile	Arg	Pro	Asp
225					230					235					240
Pro	Pro	His	Pro	Arg	Glu	Gly	Gln	Lys	Leu	Leu	Leu	His	Cys	Glu	Gly
				245					250					255	
Arg	Gly	Asn	Pro	Val	Pro	Gln	Gln	Tyr	Leu	Trp	Glu	Lys	Glu	Gly	Ser
			260					265					270		
Val	Pro	Pro	Leu	Lys	Met	Thr	Gln	Glu	Ser	Ala	Leu	Ile	Phe	Pro	Phe
		275					280					285			

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 87
cctagcacag tgacgagga cttggc 26

<210> 88
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 88
aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc 50

<210> 89
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 89
gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90
<211> 2755
<212> DNA
<213> Homo sapiens

<400> 90
ggggggttagg gaggaaggaa tccacccccca cccccccaaa ccccttttctt ctccttttctt 60
ggcttcggac attggagcac taaatgaact tgaattgtgt ctgtggcgag caggatgggc 120
gctgttactt tgtgatgaga tcggggatga attgctcgct ttaaaaatgc tgctttggat 180
tctgttgctg gagacgtctc tttgttttgc cgctggaaac gttacagggg acgtttgcaa 240
agagaagatc tgttcctgca atgagataga aggggaccta cacgtagact gtgaaaaaaaa 300
gggcttcaca agtctgcagc gtttcactgc cccgacttcc cagttttacc atttatttct 360
gcatggcaat tccctcactc gacttttccc taatgagttc gctaactttt ataatgcggt 420
tagtttgcac atggaaaaca atggcttgca tgaaatcggt ccgggggctt ttctggggct 480
gcagctgggtg aaaaggctgc acatcaacaa caacaagatc aagtcttttc gaaagcagac 540
ttttctgggg ctggacgac tggaatatct ccaggctgat tttaatttat tacgagatat 600
agaccggggg gccttcagg acttgaacaa gctggagggtg ctcattttaa atgacaatct 660
catcagcacc ctacctgcca acgtgttcca gtatgtgccc atcaccacc tgcacctccg 720
gggtaacagg ctgaaaacgc tgccctatga ggagggtcttg gagcaaatcc ctggtattgc 780
ggagatcctg ctagaggata acccttggga ctgcacctgt gatctgctct ccctgaaaga 840
atggctggaa aacattccca agaatgccct gatcggccga gtggtctgcg aagccccac 900
cagactgcag ggtaaagacc tcaatgaaac caccgaacag gacttgtgtc ctttgaaaaa 960
ccgagtggat tctagtctcc cggcgcccc tgcccaagaa gagaccttg ctctgggacc 1020
cctgccaaact cctttcaaga caaatgggca agaggatcat gccacaccag ggtctgctcc 1080

```
<210> 91
<211> 696
<212> PRT
<213> Homo sapiens
```

Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala
1 5 10 15

Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn
20 25 30

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
35 40 45

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
50 55 60

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
65 70 75 80

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
85 90 95

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His
 100 105 110
 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly
 115 120 125
 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp
 130 135 140
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile
 145 150 155 160
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr
 165 170 175
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu
 180 185 190
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu
 195 200 205
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys
 210 215 220
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val
 225 230 235 240
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr
 245 250 255
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro
 260 265 270
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr
 275 280 285
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala
 290 295 300
 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg
 305 310 315 320
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala
 325 330 335
 Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly
 340 345 350
 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala
 355 360 365
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp
 370 375 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn
 385 390 395 400
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn
 405 410 415
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser
 420 425 430
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn
 435 440 445
 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro
 450 455 460
 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn
 465 470 475 480
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu
 485 490 495
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala
 500 505 510
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly
 515 520 525
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala
 530 535 540
 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr
 545 550 555 560
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu
 565 570 575
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His
 580 585 590
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser
 595 600 605
 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu
 610 615 620
 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val
 625 630 635 640
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser
 645 650 655
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

[illegible]

gaggggaagg gagggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240
 ccagacacag ctctgcgtcc tcgagcggga cagatccaag ttgggagcag ctctgcgtgc 300
 ggggcctcag agaatgaggc cggcggttcgc cctgtgcctc ctctggcagg cgctctggcc 360
 cgggcccgggc ggcggcgaac accccaactgc cgaccgtgct ggctgctcgg cctcgggggc 420
 ctgctacagc ctgcaccacg ctaccatgaa gcggcaggcg gccgaggagg cctgcacctc 480
 gcgaggtggg gcgctcagca ccgtgcgtgc gggcgccgag ctgcgcgctg tgctcgcgct 540
 cctgcgggca gggccagggc ccggaggggg ctccaaagac ctgctgttct gggtcgcact 600
 ggagcgcagg cggtccact gcacctgga gaacgagcct ttgcgggggt tctcctggct 660
 gtcctccgac cccggcggtc tcgaaagcga cacgctgcag tgggtggagg agccccaacg 720
 ctctgcacc gcgcggagat gcgcggtact ccaggccacc ggtggggtcg agcccgagg 780
 ctggaaggag atgcgatgcc acctgcgcgc caacggctac ctgtgcaagt accagtttga 840
 ggtcttgtgt cctgcgcgcg gcccgggggc cgctctaac ttgagctatc gcgcgccctt 900
 ccagctgcac agcgcgcgctc tggacttcag tccacctggg accgaggtga gtgcgctctg 960
 ccggggacag ctcccgatct cagttacttg catcgcggac gaaatcggcg ctgcgtggga 1020
 caaactctcg ggcgatgtgt tgtgtccctg ccccgggagg tacctccgtg ctggcaaatg 1080
 cgcagagctc cctaactgcc tagacgactt gggaggcttt gcctgcgaat gtgtacggg 1140
 cttcgagctg ggggaaggac gccgctcttg tgtgaccagt ggggaaggac agccgaccct 1200
 tggggggacc ggggtgcca ccaggcgccc gccggccact gcaaccagcc ccgtgccgca 1260
 gagaacatgg ccaatcaggg tcgacgagaa gctgggagag acaccaactg tccctgaaca 1320
 agacaattca gtaacatcta ttctcgatg tctcgatgg ggatcacaga gcacgatgtc 1380
 tacccttcaa atgtcccttc aagccgagtc aaaggccact atcaccccat cagggagcgt 1440
 gatttccaag ttttaattcta cgacttctc tgccactcct caggctttcg actcctctc 1500
 tgccgtgggc ttcatatttg tgagcacagc agtagtagt ttggtgatct tgaccatgac 1560
 agtactgggg cttgtcaagc tctgctttca cgaaagccc tcttccagc caaggaagga 1620
 gtctatgggc ccgcggggc tggagagtga tctcgagccc gctgctttgg gctccagttc 1680
 tgcacattgc acaaacaatg gggtgaaagt cggggactgt gatctgcggg acagagcaga 1740
 ggggtgccttg ctggcggagt cccctcttgg ctctagtgt gcatagggaa acaggggaca 1800
 tgggcactcc tgtgaacagt ttttacttt tgatgaaacg gggaaccaag aggaacttac 1860
 ttgtgtaact gacaatttct gcagaaatcc ccttctctc aaattccctt tactccactg 1920
 aggagctaaa tcagaactgc acactcctc cctgatgata gaggaagtgg aagtgccttt 1980
 aggatggtga tactggggga ccgggtagt ctggggagag atattttct atgtttatc 2040
 ggagaatttg gagaagtgt tgaacttttc aagacattgg aaacaaatag aacacaatat 2100
 aatttacatt aaaaaataat ttctaccaa atggaaagga aatgttctat gttgttcagg 2160
 ctaggagtat attggttcga aatcccaggg aaaaaataa aaataaaaaa ttaaaggatt 2220
 gttgat 2226

<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
 1 5 10 15

Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser
 20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
 35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
 50 55 60

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly
 65 70 75 80
 Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu
 85 90 95
 Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly
 100 105 110
 Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu
 115 120 125
 Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala
 130 135 140
 Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met
 145 150 155 160
 Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu
 165 170 175
 Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr
 180 185 190
 Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro
 195 200 205
 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val
 210 215 220
 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly
 225 230 235 240
 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys
 245 250 255
 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu
 260 265 270
 Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr
 275 280 285
 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg
 290 295 300
 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro
 305 310 315 320
 Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln
 325 330 335
 Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

```
<210> 97
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
```

```
<210> 98
<211> 20
<212> DNA
<213> Artificial Sequence
```

```
<400> 98
tgaccagtgg ggaaggacag                20
```



```
<210> 103
<211> 2026
<212> DNA
<213> Homo sapiens
```

<400> 103

```

cggacgcgtg ggattcagca gtggcctgtg gctgccagag cagctectca ggggaaacta 60
agcgtcgagt cagacggcac cataatcgcc tttaaaagtg cctccgccct gccggccgcg 120
tatcccccg ctacctgggc cgccccgcgg cgggtgcgcgc gtgagaggga gcgcgcgggc 180
agccgagcgc cgggtgtgagc cagcgtctgt gccagtgtga gcggcgggtg gagecgggtg 240
ggtgcggagg ggcgtgtgtg ccggcgcgcg ccgcgtgggg tgcaaaccce gagcgtctac 300
gctgccatga ggggcgcgaa cgcttggggc ccaactctgc tgetgctggc tgccgccacc 360
cagctctcgc ggcagcagtc cccagagaga cctgttttca catgtggtgg cattcttact 420
ggagagtctg gatttatttg cagtgaaggt tttcctggag tgtaccctcc aaatagcaaa 480
tgtacttgga aaatcacagt tcccgaagga aaagtagtgc ttctcaattt ccgattcata 540
gacctcgaga gtgacaacct gtgcccgtat gactttgtgg atgtgtacaa tggccatgcc 600
aatggccagc gcattggccg cttctgtggc actttccggc ctggagccct tgtgtccagt 660
ggcaacaaga tgatggtgca gatgatttct gatgccaaac cagctggcaa tggcttcatg 720
gccatgttct ccgctgtctg accaaacgaa agaggggagc agtattgtgg aggactcctt 780
gacagacctt ccggctcttt taaaaccccc aactggccag accgggatta ccctgcagga 840
gtcacttggt tgtggcacat tgtagcccca aagaatcagc ttatagaatt aaagtttgag 900
aagtttgatg tggagcgaga taactactgc cgatatgatt atgtggctgt gtttaatggc 960
ggggaagtca acgatgctag aagaattgga aagtattgtg gtgatagtcc acctgcgcca 1020
attgtgtctg agagaaatga acttcttatt cagtttttat cagacttaag ttttaactgca 1080
gatgggttta ttggtcacta catattcagg ccaaaaaaac tgcctacaac tacagaacag 1140
cctgtcacca ccacattccc tgtaaccacg ggttttaaac ccaccgtggc cttgtgtcaa 1200
caaaagtgtg gacggacggg gactctggag ggcaattatt gttcaagtga ctttgtatta 1260
gccggcactg ttatcacaaac catcactcgc gatgggagtt tgcacgccac agtctcgatc 1320
atcaacatct acaaagaggg aaatttggcg attcagcagg cgggcaagaa catgagtgcc 1380
aggctgactg tegtctgcaa gcagtgcct ctcctcagaa gaggtctaaa ttacattatt 1440
atgggccaaag taggtgaaga tgggcgaggc aaaatcatgc caaacagctt tatcatgatg 1500
ttcaagacca agaatcagaa gctcctggat gccttaaaaa ataagcaatg ttaacagtga 1560
actgtgtcca ttttaagctgt attctgccat tgcccttgaa agatctatgt tctctcagta 1620
gaaaaaaaaa tacttataaa attacatatt ctgaaagagg attccgaaag atgggactgg 1680
ttgactcttc acatgatgga ggtatgaggc ctccgagata gctgagggaa gttctttgcc 1740
tgctgtcaga ggagcagcta tctgattgga aacctgccga cttagtgcgg tgataggaag 1800
ctaaaagtgt caagcgttga cagcttggaa gcgtttattt atacatctct gtaaaaggat 1860
attttagaat tgagttgtgt gaagatgtca aaaaaagatt ttagaagtgc aatatttata 1920
gtgttatttg tttcaccttc aagcctttgc cctgaggtgt tacaatcttg tcttgcgttt 1980
tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa 2026

```

<210> 104

<211> 415

<212> PRT

<213> Homo sapiens

<400> 104

```

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
  1              5              10              15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
      20              25              30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
      35              40              45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
      50              55              60

```

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu
 65 70 75 80
 Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
 85 90 95
 His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro
 100 105 110
 Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser
 115 120 125
 Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala
 130 135 140
 Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg
 145 150 155 160
 Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro
 165 170 175
 Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu
 180 185 190
 Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys
 195 200 205
 Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala
 210 215 220
 Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val
 225 230 235 240
 Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu
 245 250 255
 Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu
 260 265 270
 Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr
 275 280 285
 Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr
 290 295 300
 Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly
 305 310 315 320
 Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val
 325 330 335
 Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

F
O
L
D
E
D
S
E
R
I
E
S

```

<210> 105
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 105
ccgattcata gacctcgaga gt

<210> 106
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 106
gtcaaggagt cctccacaat ac

<210> 107
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 107
gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

<210> 108
<211> 1838
<212> DNA

```

45

<213> Homo sapiens

<400> 108

```

cggacgcgtg ggcggacgcg tgggcggccc acggcgcccc cgggctgggg cggtcgcttc 60
ttccttctcc gtggcctacg aggggtcccca gcctgggtaa agatggcccc atggcccccg 120
aagggcctag tcccagctgt gctctggggc ctccagcctct tcctcaacct cccaggacct 180
atctggctcc agccctctcc acctccccag tcttctcccc cgccctcagcc ccatccgtgt 240
catacctgcc ggggactggt tgacagcttt aacaagggcc tggagagAAC catccgggac 300
aactttggag gtggaaacac tgccctgggag gaagagaatt tgtccaaata caaagacagt 360
gagaccgcgc tggtagaggt gctggagggt gtgtgcagca agtcagactt cgagtgccac 420
cgccctgctg agctgagtga ggagctggtg gagagctggt ggtttcaca gcagcaggag 480
gccccggacc tcttcagtg gctgtgctca gattccctga agctctgctg ccccgaggc 540
accttcgggc cctcctgcct tccctgtcct gggggaacag agaggccctg cgggtggctac 600
gggcagtgtg aaggagaagg gacacgaggg ggcagcgggc actgtgactg ccaagccggc 660
tacgggggtg aggcctgtgg ccagtgtggc cttggctact ttgaggcaga acgcaacgcc 720
agccatctgg tatgttcggc ttgttttggc ccctgtgccc gatgctcagg acctgaggaa 780
tcaaactggt tgcaatgcaa gaagggtggt gccctgcac acctcaagtg tgtagacatt 840
gatgagtgtg gcacagaggg agccaactgt ggagctgacc aattctgcgt gaacactgag 900
ggctcctatg agtgccgaga ctgtgccaa gctgcctag gctgcatggg ggcagggcc 960
ggtcgctgta agaagtgtag ccctggctat cagcagggtg gctccaagt tctcgatgtg 1020
gatgagtgtg agacagagg gtgtccggga gagaacaagc agtgtgaaa caccgagggc 1080
ggttatcgct gcactgtgac cgagggtctc aagcagatgg aaggcatctg tgtgaaggag 1140
cagatccag agtcagcagg cttcttctca gagatgacag aagacgagtt ggtgggtgctg 1200
cagcagatgt tctttggcat catcatctgt gcactggcca cgctggctgc taaggcgac 1260
ttggtgttca ccgccatctt cattggggct gtggcgcca tgactggcta ctggttgtca 1320
gagcgcagtg accgtgtgct ggagggtctt atcaaggcca gataatcgcg gccaccacct 1380
gtaggacctc cccccacca cgctgcccc agagcttggg ctgccctcct gctggacact 1440
caggacagct tggtttattt ttgagagtgg ggtaagcacc cctacctgcc ttacagagca 1500
gcccaggtac ccaggccccg gcagacaagg cccctggggg aaaaagtagc cctgaagggtg 1560
gataccatga gctcttcacc tggcggggac tggcaggctt cacaatgtgt gaatttcaaa 1620
agtttttctt taatggtggc tgctagagct ttggccccctg cttaggatta ggtggctctc 1680
acaggggtgg ggccatcaca gctccctcct gccagctgca tgctgccagt tcctgttctg 1740
tgttcaccac atccccacac ccatttgcca cttatttatt catctcagga aataaagaaa 1800
ggtcttgga agttaaaaaa aaaaaaaaaa aaaaaaaaaa 1838

```

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

```

Met Ala Pro Trp Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
  1           5           10           15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
      20           25           30

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
      35           40           45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
      50           55           60

```

Arg	Asp	Asn	Phe	Gly	Gly	Gly	Asn	Thr	Ala	Trp	Glu	Glu	Glu	Asn	Leu	65	70	75	80
Ser	Lys	Tyr	Lys	Asp	Ser	Glu	Thr	Arg	Leu	Val	Glu	Val	Leu	Glu	Gly	85	90	95	
Val	Cys	Ser	Lys	Ser	Asp	Phe	Glu	Cys	His	Arg	Leu	Leu	Glu	Leu	Ser	100	105	110	
Glu	Glu	Leu	Val	Glu	Ser	Trp	Trp	Phe	His	Lys	Gln	Gln	Glu	Ala	Pro	115	120	125	
Asp	Leu	Phe	Gln	Trp	Leu	Cys	Ser	Asp	Ser	Leu	Lys	Leu	Cys	Cys	Pro	130	135	140	
Ala	Gly	Thr	Phe	Gly	Pro	Ser	Cys	Leu	Pro	Cys	Pro	Gly	Gly	Thr	Glu	145	150	155	160
Arg	Pro	Cys	Gly	Gly	Tyr	Gly	Gln	Cys	Glu	Gly	Glu	Gly	Thr	Arg	Gly	165	170	175	
Gly	Ser	Gly	His	Cys	Asp	Cys	Gln	Ala	Gly	Tyr	Gly	Gly	Glu	Ala	Cys	180	185	190	
Gly	Gln	Cys	Gly	Leu	Gly	Tyr	Phe	Glu	Ala	Glu	Arg	Asn	Ala	Ser	His	195	200	205	
Leu	Val	Cys	Ser	Ala	Cys	Phe	Gly	Pro	Cys	Ala	Arg	Cys	Ser	Gly	Pro	210	215	220	
Glu	Glu	Ser	Asn	Cys	Leu	Gln	Cys	Lys	Lys	Gly	Trp	Ala	Leu	His	His	225	230	235	240
Leu	Lys	Cys	Val	Asp	Ile	Asp	Glu	Cys	Gly	Thr	Glu	Gly	Ala	Asn	Cys	245	250	255	
Gly	Ala	Asp	Gln	Phe	Cys	Val	Asn	Thr	Glu	Gly	Ser	Tyr	Glu	Cys	Arg	260	265	270	
Asp	Cys	Ala	Lys	Ala	Cys	Leu	Gly	Cys	Met	Gly	Ala	Gly	Pro	Gly	Arg	275	280	285	
Cys	Lys	Lys	Cys	Ser	Pro	Gly	Tyr	Gln	Gln	Val	Gly	Ser	Lys	Cys	Leu	290	295	300	
Asp	Val	Asp	Glu	Cys	Glu	Thr	Glu	Val	Cys	Pro	Gly	Glu	Asn	Lys	Gln	305	310	315	320
Cys	Glu	Asn	Thr	Glu	Gly	Gly	Tyr	Arg	Cys	Ile	Cys	Ala	Glu	Gly	Tyr	325	330	335	
Lys	Gln	Met	Glu	Gly	Ile	Cys	Val	Lys	Glu	Gln	Ile	Pro	Glu	Ser	Ala	340	345	350	

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln
 355 360 365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys
 370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met
 385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe
 405 410 415

Ile Lys Gly Arg
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga 50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc 22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac 22

<210> 113

110-113-50-22-22

<211> 1616
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1461)
 <223> a, t, c or g

<400> 113
 tgagaccctc ctgcagcctt ctcaagggac agccccactc tgccctcttgc tccctccaggg 60
 cagcaccatg cagccccctgt ggctctgctg ggcactctgg gtgttgcccc tggccagccc 120
 cggggccgcc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180
 agaggtgccc accctggaca gggccgacat ggaggagctg gtcaccccca cccacgtgag 240
 ggcccagtac gtggccctgc tgcagcgag ccacggggac cgctcccgcg gaaagaggtt 300
 cagccagagc ttccgagagg tggccggcag gttcctggcg ttggaggcca gcacacacct 360
 gctggtgttc ggcattggagc agcggctgcc gcccaacagc gagctggtgc aggcctgtgt 420
 gcggctcttc caggagccgg tccccaaagg cgcgctgcac aggcacgggc ggctgtcccc 480
 gcgcagcgcc cggggcccggtg tgaccgtcga gtggtgtgcg gtccgcgacg acggtcccaa 540
 ccgcacctcc ctcatcgact ccaggctggt gtccgtccac gagagcggct ggaaggcctt 600
 cgacgtgacc gaggccgtga acttctggca gcagctgagc cggccccggc agcgcgtgct 660
 gctacaggtg tcggtgcaga gggagcatct gggcccgcgt gcgtccggcg cccacaagct 720
 ggtccgcttt gcctcgagg gggcgccagc cgggcttggg gagccccagc tggagctgca 780
 caccctggac cttggggact atggagctca gggcgactgt gacctgaag caccaatgac 840
 cgagggcacc cgctgctgcc gccaggagat gtacattgac ctgcagggga tgaagtgggc 900
 cgagaactgg gtgctggagc ccccgggctt cctggcttat gagtgtgtgg gcacctgccg 960
 gcagcccccg gaggccctgg ccttcaagtg gccgtttctg gggcctcgac agtgcacgcg 1020
 ctcgagact gactcgctgc ccatgatcgt cagcatcaag gagggaggca ggaccaggcc 1080
 ccaggtggtc agcctgcca acatgagggt gcagaagtgc agctgtgcct cggatggtgc 1140
 gctcgtgcca aggaggctcc agccataggc gcctagtgtg gccatcgagg gacttgactt 1200
 gtgtgtgttt ctgaagtgtt cgaggggtacc aggagagctg gcgatgactg aactgctgat 1260
 ggacaaatgc tctgtgctct ctagttagcc ctgaatttgc ttcctctgac aagttacctc 1320
 acctaatatt tgcttctcag gaatgagaat ctttggccac tggagagccc ttgctcagtt 1380
 ttctctattc ttattattca ctgcactata ttctaagcac ttacatgtgg agatactgta 1440
 acctgagggc agaaagccca ntgtgtcatt gtttacttgt cctgtcactg gatctgggct 1500
 aaagtcctcc accaccactc tggacctaa acctgggggt aagtgtgggt tgtgcacccc 1560
 caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616

<210> 114
 <211> 366
 <212> PRT
 <213> Homo sapiens

<400> 114
 Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala
 1 5 10 15
 Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu
 20 25 30
 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met
 35 40 45

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu
 50 55 60
 Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln
 65 70 75 80
 Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr
 85 90 95
 His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu
 100 105 110
 Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala
 115 120 125
 Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg
 130 135 140
 Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr
 145 150 155 160
 Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys
 165 170 175
 Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg
 180 185 190
 Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu
 195 200 205
 Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln
 210 215 220
 Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
 225 230 235 240
 Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro
 245 250 255
 Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu
 260 265 270
 Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe
 275 280 285
 Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu
 290 295 300
 Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu
 305 310 315 320
 Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr
 325 330 335

P
D
E
F
I
N
E
D
S
E
Q
U
E
N
C
E

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser
 340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro
 355 360 365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 115

aggactgccca taacttgctt g 21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 116

ataggagtgtg aagcagcgct gc 22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc 45

<210> 118

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 118

gtctgttccc aggagtcctt cggcggctgt tgtgtcagtg gctgatacgc gatggggaca 60
 aaggcgcaag tcgagaggaa actgttgtgc ctcttcatat tggcgatcct gttgtgctcc 120
 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tctgagaat 180

115 116 117 118

```

aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtgggaag 240
tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agcttcctat 300
gaggaccggg tgaccttctt gccaaactggt atcaccttca agtccgtgac acgggaagac 360
actgggacat acacttgtat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420
gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctctctgccc 480
accattggga accgggcagt gctgacatgc tcagaacaag atgggtcccc accttctgaa 540
tacacctggt tcaaagatgg gatagtgatg cctacgaatc ccaaaagcac cagtgccttc 600
agcaactctt cctatgtcct gaatcccaca acaggagagc tgggtcttga tccccgtgca 660
gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720
tcaaagtctg tgcgcatgga agctgtggag cggaatgtgg gggtcacgtg ggcagccgtc 780
cttgtaaccc tgattctcct gggaatcttg gtttttggca tctgggttgc ctatagccga 840
ggccactttg acagaacaaa gaaagggact tcgagtaaga aggtgattta cagccagcct 900
agtccccgaa gtgaaggaga attcaaacag acctcgatc tcttgggtgt agcctgggtc 960
gctcaccgcc tatcatctgc atttgcctta cttaggtgct accggactct ggccccctgat 1020
gtctgtagtt tcacaggatg ccttatttgt cttctacacc ccacagggcc cctacttct 1080
tcggatgtgt ttttaataat gtcagctatg tgccccatcc tcttcatgac cctccctccc 1140
tttcctacca ctgctgagtg gcctggaact tgtttaaagt gtttatcccc catttctttg 1200
agggatcagg aaggaatcct gggtatgcc a ttgacttccc ttctaagtag acagcaaaaa 1260
tgggcggggt cgcaggaatc tgcactcaac tgcccacctg gctggcaggg atctttgaat 1320
aggtatcttg agcttgggtc tgggctcttt ccttgtgtac tgacgaccag ggccagctgt 1380
tctagagcgg gaattagagg cttagagcggc tgaaatgggt gtttgggtgat gacactgggg 1440
tccttccatc tctggggccc actctcttct gtcttccat ggggaagtgc actgggatcc 1500
ctctgccctg tctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaaatggg 1560
agctcttgtt gtggagagca tagtaaattt tcagagaact tgaagccaaa aggattttaa 1620
accgtgctc taaagaaaag aaaactggag gctgggcgca gtggctcacg cctgtaatcc 1680
cagaggctga ggcaggcgga tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740
ggagaaaccc tactggaaat acaaagttag ccaggcatgg tgggtgcatgc ctgtagtccc 1800
agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa aaaaaaa 1857

```

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
1 5 10 15

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
20 25 30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
 100 105 110
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
 115 120 125
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
 130 135 140
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
 145 150 155 160
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
 165 170 175
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
 180 185 190
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
 195 200 205
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
 210 215 220
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
 225 230 235 240
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
 245 250 255
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
 260 265 270
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
 275 280 285
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 120

tcgcgagct gtgttctgtt tccc

24

<210> 121

<211> 50

TCGCGAGCTGTGTCTGTTC

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 121
 tgatcgcat ggggacaaag gcgcaagctc gagaggaaac tgttgtgcct 50

 <210> 122
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 122
 acacctggtt caaagatggg 20

 <210> 123
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 123
 taggaagagt tgctgaaggc acgg 24

 <210> 124
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 124
 ttgccttact caggtgctac 20

 <210> 125
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

```

<400> 125
actcagcagcgt ggtaggaaag                                     20

<210> 126
<211> 1210
<212> DNA
<213> Homo sapiens

<400> 126
cagcgcgtgg ccggcgccgc tgtgggggaca gcatgagcgg cgggttggatg gcgcaggttg 60
gagcgtggcg aacaggggct ctgggccttg cgctgctgct gctgctcggc ctccgactag 120
gcctggaggc cgccgcgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180
gtcagggctc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtga 300
ggattgagcc atgtacccag aaagggcaat gccaccgcc ccttggcctc ccttgcctct 360
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccaactcacgt 480
ggcgctgcga cggccaccca gactgtccc actccagcga cgagctcggc tgtggaacca 540
atgagatcct cccggaaggg gatgccacaa ccatggggcc ccttgtgacc ctggagagtg 600
tcacctctct caggaatgcc acaaccatgg ggccccctgt gaccctggag agtgtccctt 660
ctgtcgggaa tgccacatcc tcctctgccc gagaccagtc tggaaagcca actgcctatg 720
gggttattgc agctgctgcg gtgctcagtg caagcctggt caccgccacc ctctctcttt 780
tgtcctggct ccgagcccag gagcgccctc gccactggg gttactggtg gccatgaagg 840
agtccctgct gctgtcagaa cagaagacct cgctgccctg aggacaagca cttgccacca 900
ccgtcactca gccctgggcg tagccggaca ggaggagagc agtgatgcgg atgggtacct 960
gggcacacca gccctcagag acctgagttc ttctggccac gtggaacctc gaacccgagc 1020
tcctgcagaa gtggcccttg agattgaggg tccttggaac ctccctatgg agatccgggg 1080
agctaggatg gggaacctgc cacagccaga actgagggggc tggccccagg cagctcccag 1140
ggggtagaac ggccctgtgc ttaagacact ccttgttgcc ccgtctgagg gtggcgatta 1200
aagtgtcttc                                     1210

<210> 127
<211> 282
<212> PRT
<213> Homo sapiens

<400> 127
Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala
  1           5           10           15
Leu Gly Leu Ala Leu Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
          20           25           30
Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
          35           40           45
Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
          50           55           60
Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
          65           70           75           80

```

<210> 129

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 129

ttggttccac agccgagctc gtcg

24

<210> 130

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 130

gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc

50

<210> 131

<211> 1843

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (1837)

<223> a, t, c or g

<400> 131

```

cccacgcgct cgggtctcgct cgctcgcgca gcggcggcag cagaggtcgc gcacagatgc 60
gggttagact ggcgggggga ggaggcggag gagggaagga agctgcatgc atgagacca 120
cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccoga 180
gcaatggaga tggatttcta gaggcagcag agcagcagca gcaacctcag tccccccaga 240
gactcttggc cgtgatcctg tggtttcagc tggcgtgtg cttcgccct gcacagctca 300
cgggcggggt cgatgacctt caagtgtgtg ctgaccccg cttcccgag aatggcttca 360
ggacccccag cggagggggt tcttttgaag gctctgtagc ccgatttcac tgccaagacg 420
gattcaagct gaaggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480
gctggatccc aagtataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaactc 540
aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgct 600
atgaaggatt caagatccgg taccgccgac tacacaatat ggtttcatta tgtcgcgatg 660
atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720
atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780
atcgtgctt tcccgattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840
ttatctggtc gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900
ctccaatggt ggtcacgga gatttcgtct gccaccgcg gccttgtgag cgctacaacc 960
acggaactgt ggtggagttt tactgcgata ctggctacag cctcaccagc gactacaagt 1020
acatcacctg ccagtatgga gagtggtttc cttcttatca agtctactgc atcaaactcag 1080
agcaaacgtg gccagcacc catgagaccc tcccgaccac gtggaagatt gtggcggttca 1140

```


			180				185				190					
Ile	Ser	Glu	Leu	Gln	Thr	Ser	Phe	Pro	Val	Gly	Thr	Val	Ile	Ser	Tyr	
		195					200					205				
Arg	Cys	Phe	Pro	Gly	Phe	Lys	Leu	Asp	Gly	Ser	Ala	Tyr	Leu	Glu	Cys	
		210				215					220					
Leu	Gln	Asn	Leu	Ile	Trp	Ser	Ser	Ser	Pro	Pro	Arg	Cys	Leu	Ala	Leu	
225					230					235						240
Glu	Ala	Gln	Val	Cys	Pro	Leu	Pro	Pro	Met	Val	Ser	His	Gly	Asp	Phe	
				245					250				255			
Val	Cys	His	Pro	Arg	Pro	Cys	Glu	Arg	Tyr	Asn	His	Gly	Thr	Val	Val	
			260					265					270			
Glu	Phe	Tyr	Cys	Asp	Pro	Gly	Tyr	Ser	Leu	Thr	Ser	Asp	Tyr	Lys	Tyr	
		275					280					285				
Ile	Thr	Cys	Gln	Tyr	Gly	Glu	Trp	Phe	Pro	Ser	Tyr	Gln	Val	Tyr	Cys	
		290				295					300					
Ile	Lys	Ser	Glu	Gln	Thr	Trp	Pro	Ser	Thr	His	Glu	Thr	Leu	Leu	Thr	
305					310					315						320
Thr	Trp	Lys	Ile	Val	Ala	Phe	Thr	Ala	Thr	Ser	Val	Leu	Leu	Val	Leu	
			325						330					335		
Leu	Leu	Val	Ile	Leu	Ala	Arg	Met	Phe	Gln	Thr	Lys	Phe	Lys	Ala	His	
			340					345					350			
Phe	Pro	Pro	Arg	Gly	Pro	Pro	Arg	Ser	Ser	Ser	Ser	Asp	Pro	Asp	Phe	
		355					360					365				
Val	Val	Val	Asp	Gly	Val	Pro	Val	Met	Leu	Pro	Ser	Tyr	Asp	Glu	Ala	
		370				375					380					
Val	Ser	Gly	Gly	Leu	Ser	Ala	Leu	Gly	Pro	Gly	Tyr	Met	Ala	Ser	Val	
385					390					395						400
Gly	Gln	Gly	Cys	Pro	Leu	Pro	Val	Asp	Asp	Gln	Ser	Pro	Pro	Ala	Tyr	
				405					410					415		
Pro	Gly	Ser	Gly	Asp	Thr	Asp	Thr	Gly	Pro	Gly	Glu	Ser	Glu	Thr	Cys	
			420					425					430			
Asp	Ser	Val	Ser	Gly	Ser	Ser	Glu	Leu	Leu	Gln	Ser	Leu	Tyr	Ser	Pro	
		435					440					445				
Pro	Arg	Cys	Gln	Glu	Ser	Thr	His	Pro	Ala	Ser	Asp	Asn	Pro	Asp	Ile	
		450				455					460					

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn
 485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 133

atctcctatc gctgctttcc cgg

23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc

23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 135

atttaaactt gatgggtctg cgtatcttga gtgcttaca aaccttatct

50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

cccacgcgtc cgctccgcgc cctccccccc gctcccgctg cggtcgcgtc gtggcctaga 60
 gatgctgctg ccgcggttgc agttgtcgcg cagcctctg cccgccagcc cgctccaccg 120
 ccgtagcgcg cgagtgtcgg ggggcgcacc cgagtgcggc catgaggccg ggaaccgcgc 180
 tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtcgctgc 240
 tgagtgcctc ggatttgac ctgagaggag ggcagccagt ctgccgggga gggacacaga 300

136-1815

```

ggccttgtaa taaagtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360
ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420
agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatggtgac ttctggattg 480
ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcgga 600
gcgaggtctg cgtgggtcatg taccatcagc catcggcacc cgctggcatc ggaggcccct 660
acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaatatt 720
ctgatgagaa accagcagtt ctttctagag aagctgaagg tgaggaaaca gagctgacaa 780
cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840
gagaagctgc cttgaatctg gcctacatcc taatccccag cattccccct ctcctcctcc 900
ttgtgggtcac cacagttgta tgttgggttt ggatctgtag aaaaagaaaa cgggagcagc 960
cagaccctag caciaaagaag caacacacca tctggccctc tcctcaccag ggaaacagcc 1020
cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagaccc 1080
ggccagacct gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140
tgtcttgtga ctatgacaac atggctgtga acccatcaga aagtgggttt gtgactctgg 1200
tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccca gaccaaattg 1260
ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacatataaa 1320
aaactgaaac tgacaacaat ggaaaagaaa tgataagcaa aatcctctta ttttctataa 1380
ggaaaataca cagaaggtct atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440
tccccacgac ctctgtttg acccccacgt tttggctgta tcctttatcc cagccagtca 1500
tccagctcga ctttatgaga aggtaccttg ccaggtctg gcacatagta gagtctcaat 1560
aaatgtcact tggttggttg tatctaactt ttaagggaca gagctttacc tggcagtgat 1620
aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680
atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740
ttggcctgtg catcggaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800
agcaggaaaa aaaaa 1815

```

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser
65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn
85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
100 105 110

<210> 138

<211> 50
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 138
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 139
 aagccaaaga agcctgcagg aggg 24

<210> 140

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 140
 cagtccaagc ataaagggtcc tggc 24

<210> 141

<211> 1514

<212> DNA

<213> Homo sapiens

<400> 141

ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60
 gcatccgcag gttcccgcgg acttgggggc gcccgctgag ccccgccgcc cgcagaagac 120
 ttgtgtttgc ctctgcagc ctcaaccggg agggcagcga gggcctacca ccatgatcac 180
 tgggtgtgttc agcatgcgct tgtggacccc agtgggcgct ctgacctcgc tggcgactcg 240
 cctgcaccag cggcgggtgg ccctggccga gctgcaggag gccgatggcc agtgtccggt 300
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggctcgtg ttctgacacg gggctcggag 360
 tcctctcaag ccgctcccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420
 cccaccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaaccata 480
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540
 gctgaccaag gtgggcatgc agcaaattgt tgccttggga gagagactga ggaagaacta 600
 tgtggaagac attccctttc ttccaccaac cttcaaccga caggaggtct ttattcggtc 660
 cactaacatt tttcggaatc tggagtccac ccgttgtttg ctggctgggc ttttccagtg 720


```
<210> 143
<211> 24
<212> DNA
<213> Artificial Sequence
```


<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 144

gcagctctat taccacggga agga

24

<210> 145

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 145

tccttcccgt ggtaatagag ctgc

24

<210> 146

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 146

ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg

45

<210> 147

<211> 1686

<212> DNA

<213> Homo sapiens

<400> 147

ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60
cttaaatttc agtcatcac cttcacctgc cttgggtcatg gctctgctat tctccttgat 120
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtggg 180

400-147-567000

```
<210> 148
<211> 347
<212> PRT
<213> Homo sapiens
```

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly
1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr
100 105 110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
 115 120 125
 Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
 130 135 140
 Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
 145 150 155 160
 Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys
 165 170 175
 Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
 180 185 190
 Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
 195 200 205
 Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
 210 215 220
 Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
 225 230 235 240
 Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
 245 250 255
 Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
 260 265 270
 Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
 275 280 285
 Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly
 290 295 300
 Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln
 305 310 315 320
 Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr
 325 330 335
 His Gln Glu Asp Val Ala Val Ile Cys Ser Val
 340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 149

ttcagctcat caccttcacc tgcc

24

<210> 150

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 150

ggctcataca aaataccact aggg

24

<210> 151

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 151

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt

50

<210> 152

<211> 1427

<212> DNA

<213> Homo sapiens

<400> 152

actgcactcg gttctatcga ttgaattccc cgggggatcct ctagagatcc ctcgacctcg 60
 acccacgcgt ccgcggacgc gtggggcgac gcgtgggccc gctaccagga agagtctgcc 120
 gaaggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tggtcggctg 180
 cctgggcgtc ttcggcctct tccggtgct gcagtgggtg cgcgggaagg cctacctgcg 240
 gaatgctgtg gtggtgatca caggcgccac ctgaggctg ggcaaagaat gtgcaaaagt 300
 cttctatgct gcgggtgcta aactggtgct ctgtggccgg aatggtgggg ccctagaaga 360
 gctcatcaga gaacttaccg cttctcatgc caccaagggtg cagacacaca agccttactt 420
 ggtgaccttc gacctcacag actctggggc catagttgca gcagcagctg agatcctgca 480
 gtgctttggc tatgtcgaca tacttgtcaa caatgctggg atcagctacc gtggtaccat 540
 catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccgagt 600
 tgctctaacg aaagcactcc tgccctccat gatcaagagg aggcaaggcc acattgtcgc 660
 catcagcagc atccagggca agatgagcat tccttttcga tcagcatatg cagcctccaa 720
 gcacgcaacc caggetttct ttgactgtct gcgtgccgag atggaacagt atgaaattga 780
 ggtgaccgtc atcagccccg gctacatcca caccaacctc tctgtaaagt ccatcaccgc 840
 ggatggatct aggtatggag ttatggacac caccacagcc caggggccga gccctgtgga 900
 ggtggcccgat gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960
 cttactgcct tccttggtcg tttatcttcg aactctggct cctgggctct tcttcagcct 1020
 catggcctcc agggccagaa aagagcggaa atccaagaac tcctagtact ctgaccagcc 1080

```
<210> 153
<211> 310
<212> PRT
<213> Homo sapiens
```

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
1 5 10 15

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
35 40 45

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
65 70 75 80

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
100 105 110

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
130 135 140

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
165 170 175

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

210	215	220
Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg		
225	230	235 240
Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu		
	245	250 255
Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val		
	260	265 270
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu		
	275	280 285
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu		
	290	295 300

Arg Lys Ser Lys Asn Ser
305 310

<210> 154
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 154
gggtgctaaac tggtgctctg tggc

24

<210> 155
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 155
cagggcaaga tgagcattcc

20

<210> 156
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

154-156-157-158-159-160-161-162-163-164-165-166-167-168-169-170-171-172-173-174-175-176-177-178-179-180-181-182-183-184-185-186-187-188-189-190-191-192-193-194-195-196-197-198-199-200-201-202-203-204-205-206-207-208-209-210-211-212-213-214-215-216-217-218-219-220-221-222-223-224-225-226-227-228-229-230-231-232-233-234-235-236-237-238-239-240-241-242-243-244-245-246-247-248-249-250-251-252-253-254-255-256-257-258-259-260-261-262-263-264-265-266-267-268-269-270-271-272-273-274-275-276-277-278-279-280-281-282-283-284-285-286-287-288-289-290-291-292-293-294-295-296-297-298-299-300-301-302-303-304-305-306-307-308-309-310-311-312-313-314-315-316-317-318-319-320-321-322-323-324-325-326-327-328-329-330-331-332-333-334-335-336-337-338-339-340-341-342-343-344-345-346-347-348-349-350-351-352-353-354-355-356-357-358-359-360-361-362-363-364-365-366-367-368-369-370-371-372-373-374-375-376-377-378-379-380-381-382-383-384-385-386-387-388-389-390-391-392-393-394-395-396-397-398-399-400-401-402-403-404-405-406-407-408-409-410-411-412-413-414-415-416-417-418-419-420-421-422-423-424-425-426-427-428-429-430-431-432-433-434-435-436-437-438-439-440-441-442-443-444-445-446-447-448-449-450-451-452-453-454-455-456-457-458-459-460-461-462-463-464-465-466-467-468-469-470-471-472-473-474-475-476-477-478-479-480-481-482-483-484-485-486-487-488-489-490-491-492-493-494-495-496-497-498-499-500-501-502-503-504-505-506-507-508-509-510-511-512-513-514-515-516-517-518-519-520-521-522-523-524-525-526-527-528-529-530-531-532-533-534-535-536-537-538-539-540-541-542-543-544-545-546-547-548-549-550-551-552-553-554-555-556-557-558-559-560-561-562-563-564-565-566-567-568-569-570-571-572-573-574-575-576-577-578-579-580-581-582-583-584-585-586-587-588-589-590-591-592-593-594-595-596-597-598-599-600-601-602-603-604-605-606-607-608-609-610-611-612-613-614-615-616-617-618-619-620-621-622-623-624-625-626-627-628-629-630-631-632-633-634-635-636-637-638-639-640-641-642-643-644-645-646-647-648-649-650-651-652-653-654-655-656-657-658-659-660-661-662-663-664-665-666-667-668-669-670-671-672-673-674-675-676-677-678-679-680-681-682-683-684-685-686-687-688-689-690-691-692-693-694-695-696-697-698-699-700-701-702-703-704-705-706-707-708-709-710-711-712-713-714-715-716-717-718-719-720-721-722-723-724-725-726-727-728-729-730-731-732-733-734-735-736-737-738-739-740-741-742-743-744-745-746-747-748-749-750-751-752-753-754-755-756-757-758-759-760-761-762-763-764-765-766-767-768-769-770-771-772-773-774-775-776-777-778-779-780-781-782-783-784-785-786-787-788-789-790-791-792-793-794-795-796-797-798-799-800-801-802-803-804-805-806-807-808-809-810-811-812-813-814-815-816-817-818-819-820-821-822-823-824-825-826-827-828-829-830-831-832-833-834-835-836-837-838-839-840-841-842-843-844-845-846-847-848-849-850-851-852-853-854-855-856-857-858-859-860-861-862-863-864-865-866-867-868-869-870-871-872-873-874-875-876-877-878-879-880-881-882-883-884-885-886-887-888-889-890-891-892-893-894-895-896-897-898-899-900-901-902-903-904-905-906-907-908-909-910-911-912-913-914-915-916-917-918-919-920-921-922-923-924-925-926-927-928-929-930-931-932-933-934-935-936-937-938-939-940-941-942-943-944-945-946-947-948-949-950-951-952-953-954-955-956-957-958-959-960-961-962-963-964-965-966-967-968-969-970-971-972-973-974-975-976-977-978-979-980-981-982-983-984-985-986-987-988-989-990-991-992-993-994-995-996-997-998-999-1000

24

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

50

```
<210> 158
<211> 1771
<212> DNA
<213> Homo sapiens
```

<400> 158						
cccacgcgtc	cgctgggtgtt	agatcgagca	accctctaaa	agcagtttag	agtggtaaaa	60
aaaaaaaaaa	acacaccaaa	cgctcgcagc	cacaaaaggg	atgaaatttc	ttctggacat	120
cctcctgctt	ctcccgttac	tgatcgtctg	ctccctagag	tccttcgtga	agctttttat	180
tcctaagagg	agaaaatcag	tcaccggcga	aatcgtgctg	attacaggag	ctgggcatgg	240
aattgggaga	ctgactgcct	atgaatttgc	taaacttaaa	agcaagctgg	ttctctggga	300
tataaataag	catggactgg	aggaaaacagc	tgccaaatgc	aagggaactgg	gtgccaaagg	360
tcataacctt	gtggtagact	gcagcaaccg	agaagatatt	tacagctctg	caaagaagg	420
gaaggcagaa	attggagatg	ttagtatatt	agtaaataat	gctgggtgta	tctatacatc	480
agatttgttt	gctacacaag	atcctcagat	tgaaaagact	tttgaagtta	atgtacttgc	540
acatttctgg	actacaaaag	catttcttgc	tgcaatgacg	aagaataacc	atggccatat	600
tgctactgtg	gcttcggcag	ctggacatct	ctcggcccc	ttcttactgg	cttactgttc	660
aagaacgttt	gctcgtgttg	gatttccata	aactttgaca	gatgaactgg	ctgccttaca	720
atacaactgga	gtcaaaaaca	catgtctgtg	tcctaatttc	gtaaacactg	gcttcatcaa	780
aaatccaagt	acaagtttgg	gaccactctt	ggaacctgag	gaagtggtaa	acaggctgat	840
gcatgggatt	ctgactgagc	agaagatgat	ttttattcca	tcttctatag	cttttttaac	900
aacattggaa	aggatccttc	ctgagcgttt	cctggcagtt	ttaaaacgaa	aaatcagtgt	960
taagtttgat	gcagttattg	gatataaaat	gaaagcgcaa	taagcaccta	gttttctgaa	1020
aactgattta	ccaggtttag	gttgatgtca	tctaatagtg	ccagaatttt	aatgtttgaa	1080
cttctgtttt	ttctaattat	cccattttct	tcaatatcat	ttttgaggct	ttggcagttc	1140
tcattttacta	ccacttgttc	tttagccaaa	agctgattac	atatgatata	aacagagaaa	1200
tacctttaga	ggtgacttta	aggaaaatga	agaaaaagaa	ccaaaatgac	tttattaaaa	1260
taattttccaa	gattattttg	ggctcacctg	aaggctttgc	aaaatttgta	ccataaccgt	1320
ttattttaaca	tatattttta	tttttgattg	cacttaaatt	ttgtataatt	tgtgtttctt	1380
tttctgttct	acataaaaat	agaaacttca	agctctctaa	ataaaatgaa	ggactatatc	1440
tagtggtatt	tcacaatgaa	tatcatgaac	tctcaatggg	taggtttcat	cctaccattt	1500
gccactctgt	ttcctgagag	atacctcaca	ttccaatgcc	aaacatttct	gcacagggaa	1560
gctagagggt	gatacacgtg	ttgcaagtat	aaaagcatca	ctgggattta	aggagaattg	1620
agagaatgta	cccacaaatg	gcagcaataa	taaatggatc	acacttaaaa	aaaaaaaaaa	1680
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1740
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	a			1771

<210> 159

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile
 260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys
 275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
 290 295 300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 160

ggtgaaggca gaaattggag atg

23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 161

atcccatgca tcagcctggt tacc

24

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 162

gctggtgtag tctatacatc agatttggtt gctacacaag atcctcag

48

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

cccacgcgtc cgcggacgcg tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60
 tcaggggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaagggtg 120

160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

attgtttcgc tggctcctggt gatgcctggc ccctgtgatg ggctgtttcg ctccctatac 180
 agaagtgttt ccatgccacc taaggagagc tcaggacagc cattatttct caccctttac 240
 attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggtcggccc tttcccagga 300
 ctgaacatga agagttatgc cggcttcctc accgtgaata agacttacaa cagcaacctc 360
 ttctttctggt tcttcccagc tcagatacag ccagaagatg ccccagtagt tctctggcta 420
 caggggtgggc cgggaggttc atccatgttt ggactctttg tggaacatgg gcctttatgtt 480
 gtcacaagta acatgacctt gcgtgacaga gacttcccct ggaccacaac gctctccatg 540
 ctttacattg acaatccagt gggcacaggc ttcagtttta ctgatgatac ccacggatat 600
 gcagtcaatg aggacgatgt agcacgggat ttatacagt cactaattca gtttttccag 660
 atatttcctg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcagggaaa 720
 tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780
 aacctgaacg gaattgctat tggagatgga tattctgatc ccgaatcaat tatagggggc 840
 tatgcagaat tcctgtacca aattggcttg ttggatgaga agcaaaaaaa gtacttccag 900
 aagcagtgcc atgaatgcat agaacacatc aggaagcaga actggtttga ggcttttgaa 960
 atactggata aactactaga tggcgactta acaagtgatc cttcttactt ccagaatgtt 1020
 acaggatgta gtaattacta taactttttg cgggtgcacgg aacctgagga tcagctttac 1080
 tatgtgaaat ttttgtcact cccagaggtg agacaagcca tccacgtggg gaatcagact 1140
 tttaatgatg gaactatagt tgaaaagtc ttgcgagaag atacagtaca gtcagttaag 1200
 ccatggttaa ctgaaatcat gaataattat aaggttctga tctacaatgg ccaactggac 1260
 atcatcgtgg cagctgccct gacagagcgc tccttgatgg gcatggactg gaaaggatcc 1320
 caggaatata agaaggcaga aaaaaaagtt tggaagatct ttaaactctga cagtgaagtg 1380
 gctggttaca tccggcaagc gggtgacttc catcaggtaa ttattcgagg tggaggacat 1440
 attttaccct atgaccagcc tctgagagct tttgacatga ttaatcgatt catttatgga 1500
 aaaggatggg atccttatgt tggataaact accttcccaa aagagaacat cagaggtttt 1560
 cattgctgaa aagaaaatcg taaaaacaga aaatgtcata ggaataaaaa aattatcttt 1620
 tcatactctg aagatttttt tcatcaataa aaattatcct tgaaacaagt gagcttttgt 1680
 ttttgggggg agatgtttac tacaaaatta acatgagtac atgagtaaga attacattat 1740
 ttaacttaaa ggatgaaaag tatggatgat gtgacactga gacaagatgt ataaatgaaa 1800
 ttttaggggtc ttgaatagga agtttttaatt tcttctaaga gtaagtgaag agtgcagttg 1860
 taacaaacaa agctgtaaca tctttttctg ccaataacag aagtttggca tgccgtgaag 1920
 gtgttttgaa atattatttg ataagaatag ctcaattatc ccaaataaat ggatgaagct 1980
 ataatagttt tggggaaaaa attctcaaat gtataaagtc ttagaacaaa agaattcttt 2040
 gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
 1 5 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
 20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
 35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
 50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65					70					75				80	
Asn	Lys	Thr	Tyr	Asn	Ser	Asn	Leu	Phe	Phe	Trp	Phe	Phe	Pro	Ala	Gln
				85					90					95	
Ile	Gln	Pro	Glu	Asp	Ala	Pro	Val	Val	Leu	Trp	Leu	Gln	Gly	Gly	Pro
			100					105					110		
Gly	Gly	Ser	Ser	Met	Phe	Gly	Leu	Phe	Val	Glu	His	Gly	Pro	Tyr	Val
		115					120					125			
Val	Thr	Ser	Asn	Met	Thr	Leu	Arg	Asp	Arg	Asp	Phe	Pro	Trp	Thr	Thr
	130					135					140				
Thr	Leu	Ser	Met	Leu	Tyr	Ile	Asp	Asn	Pro	Val	Gly	Thr	Gly	Phe	Ser
145					150					155					160
Phe	Thr	Asp	Asp	Thr	His	Gly	Tyr	Ala	Val	Asn	Glu	Asp	Asp	Val	Ala
				165					170					175	
Arg	Asp	Leu	Tyr	Ser	Ala	Leu	Ile	Gln	Phe	Phe	Gln	Ile	Phe	Pro	Glu
			180					185					190		
Tyr	Lys	Asn	Asn	Asp	Phe	Tyr	Val	Thr	Gly	Glu	Ser	Tyr	Ala	Gly	Lys
		195					200					205			
Tyr	Val	Pro	Ala	Ile	Ala	His	Leu	Ile	His	Ser	Leu	Asn	Pro	Val	Arg
	210					215					220				
Glu	Val	Lys	Ile	Asn	Leu	Asn	Gly	Ile	Ala	Ile	Gly	Asp	Gly	Tyr	Ser
225					230					235					240
Asp	Pro	Glu	Ser	Ile	Ile	Gly	Gly	Tyr	Ala	Glu	Phe	Leu	Tyr	Gln	Ile
				245					250					255	
Gly	Leu	Leu	Asp	Glu	Lys	Gln	Lys	Lys	Tyr	Phe	Gln	Lys	Gln	Cys	His
			260					265					270		
Glu	Cys	Ile	Glu	His	Ile	Arg	Lys	Gln	Asn	Trp	Phe	Glu	Ala	Phe	Glu
		275					280					285			
Ile	Leu	Asp	Lys	Leu	Leu	Asp	Gly	Asp	Leu	Thr	Ser	Asp	Pro	Ser	Tyr
	290					295					300				
Phe	Gln	Asn	Val	Thr	Gly	Cys	Ser	Asn	Tyr	Tyr	Asn	Phe	Leu	Arg	Cys
305					310					315					320
Thr	Glu	Pro	Glu	Asp	Gln	Leu	Tyr	Tyr	Val	Lys	Phe	Leu	Ser	Leu	Pro
				325					330					335	
Glu	Val	Arg	Gln	Ala	Ile	His	Val	Gly	Asn	Gln	Thr	Phe	Asn	Asp	Gly
			340					345					350		

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
465 470 475

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

ttccatgcca cctaagggag actc

24

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

tggatgaggt gtgcaatggc tggc

24

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 167

agctctcaga ggctgggtcat aggg

24

<210> 168

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 168

gtcgggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac

50

<210> 169

<211> 2477

<212> DNA

<213> Homo sapiens

<400> 169

```

cgagggtctt tccgggtccg gaatggcaca tgtgggaatc ccagtcttgt tggctacaac 60
atctttccct ttcctaacaa gttctaacag ctgttctaac agctagtgat caggggttct 120
tcttgctgga gaagaaaggg ctgagggcag agcagggcac tctcactcag ggtgaccagc 180
tccttgccctc tctgtggata acagagcatg agaaagtga gagatgcagc ggagtgaggt 240
gatggaagtc taaaatagga aggaattttg tgtgcaatat cagactctgg gagcagttga 300
cctggagagc ctggggggagg gcctgcctaa caagctttca aaaaacagga ggcacttcca 360
ctgggctggg ataagacgtg ccggtaggat agggaagact ggggttagtc ctaatatcaa 420
attgactggc tgggtgaact tcaacagcct tttaacctct ctgggagatg aaaacgatgg 480
cttaaggggc cagaaataga gatgctttgt aaaataaaat tttaaaaaaa gcaagtattt 540
tatagcataa aggctagaga ccaaaataga taacaggatt ccctgaacat tcctaagagg 600
gagaaagtat gttaaaaata gaaaaaccaa aatgcagaag gaggagactc acagagctaa 660
accaggatgg ggaccctggg tcaggccagc ctctttgctc ctcccggaaa ttatttttgg 720
tctgaccact ctgccttggt ttttgcagaa tcatgtgagg gccaacgggg gaaggtggag 780
cagatgagca cacacaggag ccgtctctc accgccgcc ctctcagcat ggaacagagg 840
cagccctggc cccgggccct ggaggtggac agccgctctg tggctctgct ctcagtggtc 900
tgggtgctgc tggccccccc agcagccggc atgcctcagt tcagcacctt ccactctgag 960
aatcgtgact ggaccttcaa ccacttgacc gtccaccaag ggacgggggc cgtctatgtg 1020
ggggccatca accgggtcta taagctgaca ggcaacctga ccatccaggt ggctcataag 1080
acagggccag aagaggacaa caagtctcgt taccgcccc tcatcgtgca gccctgcagc 1140
gaagtgtca ccctcaccaa caatgtcaac aagctgctca tcattgacta ctctgagaac 1200
cgctgtctgg cctgtgggag cctctaccag ggggtctgca agctgtgctg gctggatgac 1260
ctcttcatcc tgggtggagc atcccacaag aaggagcact acctgtccag tgtcaacaag 1320
acgggcacca tgtacggggg gattgtgcgc tctgaggggt aggatggcaa gctcttcac 1380
ggcacggctg tggatgggaa gcaggattac tccccagccc tgtccagccg gaagctgccc 1440
cgagaccctg agtcttcagc catgctcgac tatgagctac acagcgattt tgtctcctct 1500
ctcatcaaga tcccttcaga caccctggcc ctgggtctccc actttgacat cttctacatc 1560
tacggctttg ctagtggggg ctttgtctac tttctcacct tccagcccga gaccctgag 1620
ggtgtggcca tcaactccgc tggagacctc ttctacacct cacgcacgt gcggctctgc 1680

```


Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys
 180 185 190
 Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys
 195 200 205
 Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly
 210 215 220
 Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr
 225 230 235 240
 Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys
 245 250 255
 Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His
 260 265 270
 Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala
 275 280 285
 Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly
 290 295 300
 Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val
 305 310 315 320
 Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg
 325 330 335
 Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe
 340 345 350
 Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr
 355 360 365
 Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser
 370 375 380
 Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr
 385 390 395 400
 His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala
 405 410 415
 Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu
 420 425 430
 Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr
 435 440 445
 Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

450 455 460
 Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr
 465 470 475 480
 Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly
 485 490 495
 Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val
 500 505 510
 Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys
 515 520 525
 Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln
 530 535 540
 Leu Tyr Phe Leu Gly Glu Gln Arg
 545 550

<210> 171

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 171

tggaataccg cctcctgcag

20

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 172

cttctgccct ttggagaaga tggc

24

<210> 173

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

42

```
<220>
<221> modified_base
<222> (1683)
<223> a, t, c or g
```

<400>	174					
aggctcccgc	gcgcggctga	gtgcggactg	gagtgggaac	ccgggtcccc	gcgcttagag	60
aacacgcgat	gaccacgtgg	agcctccggc	ggaggccggc	ccgcacgctg	ggactcctgc	120
tgctggtcgt	cttgggcttc	ctggtgctcc	gcaggctgga	ctggagcacc	ctggctccctc	180
tgcggtccg	ccatcgacag	ctggggctgc	aggccaaggg	ctggaacttc	atgctggagg	240
attccacctt	ctggatcttc	gggggctcca	tccactattt	ccgtgtgccc	agggagttact	300
ggaggggaccg	cctgctgaag	atgaaggcct	gtggcttgaa	caccctcacc	acctatgttc	360
cgtggaacct	gcatgagcca	gaaagaggca	aatttgactt	ctctgggaac	ctggacctgg	420
aggccttcgt	cctgatggcc	gcagagatcg	ggctgtgggt	gattctgcgt	ccaggccctc	480
acatctgcag	tgagatggac	ctcgggggct	tgcccagctg	gctactccaa	gacctggcca	540
tgaggctgag	gacaacttac	aagggcttca	ccgaagcagt	ggacctttat	tttgaccacc	600
tgagtaccag	ggtggtgcca	ctccagtaca	agcgtggggg	acctatcatt	gccgtgcagg	660
tggagaatga	atatggttcc	tataataaag	accccgcata	catgccctac	gtcaagaagg	720
cactggagga	ccgtggcatt	gtggaactgc	tcttgacttc	agacaacaag	gatgggctga	780
gcaaggggat	tgtccaggga	gtcttgacca	ccatcaactt	gcagtcaaca	cacgagctgc	840
agctactgac	cacctttctc	ttcaacgtcc	aggggactca	gcccgaagatg	gtgatggagt	900
actggacggg	gtggtttgac	togtggggag	gccctcacia	tatcttggat	tcttctgagg	960
tttgaaaac	cgtgtctgcc	attgtggacg	ccggctcctc	catcaacctc	tacatgttcc	1020
acggaggcac	caactttggc	ttcatgaatg	gagccatgca	cttccatgac	tacaagtcag	1080
atgtcaccag	ctatgactat	gatgctgtgc	tgacagaagc	cggcgattac	acggccaagt	1140
acatgaagct	tcgagacttc	ttcggtcca	tctcaggcat	ccctctccct	ccccacctg	1200
accttcttcc	caagatgccg	tatgagccct	taacgccagt	cttgtaactg	tctctgtggg	1260
acgccctcaa	gtacctgggg	gagccaatca	agctgaaaaa	gcccataaac	atgtgagaacc	1320
tgccagtc	tggggaaat	ggcagctcct	tcgggtacat	tctctatgag	accagcatca	1380
ctcgtctgg	catcctcagt	ggccacgtgc	atgatcgggg	gcagggtgtt	gtgaacacag	1440
tatccatagg	attcttggac	tacaagacaa	cgaagattgc	tgtccccctg	atccagggtt	1500
acaccgtgct	gaggatcttg	gtggagaatc	gtgggcgagt	caactatggg	gagaatattg	1560
atgaccagcg	caaaggctta	attggaaatc	tctatctgaa	tgattcacc	ctgaaaaact	1620
tcagaatcta	tagcctggat	atgaagaaga	gcttctttca	gagggtccgg	ctggacaaat	1680
ggngttccct	cccagaaaca	cccacattac	ctgctttctt	cttgggtagc	ttgtccatca	1740
gtccacgcc	ttgtgacacc	tttctgaagc	tggagggctg	ggagaagggg	gttgatttca	1800
tcaatggcca	gaaccttgga	cgttactgga	acattggacc	ccagaagacg	ctttacctcc	1860
caggctccctg	gttgagcagc	ggaatcaacc	aggtcatcgt	ttttgaggag	acgatggcgg	1920
gccctgcatt	acagttcacg	gaaaccccc	acctgggcag	gaaccagtac	attaagttag	1980
cgggtggcacc	ccctcctgct	ggtgccagtg	ggagactgcc	gcctcctctt	gacctgaagc	2040
ctggtggctg	ctgccccacc	cctcactgca	aaagcatctc	cttaagtaga	aacctcaggg	2100
actgggggct	acagctgccc	ctcgtctcag	ctcaaaaccc	taagcctgca	gggaaaggtg	2160
ggatggctct	gggcctggct	ttgttgatga	tggctttcct	acagccctgc	tcttgtgcgg	2220
agqctgtcgg	gctgtctcta	gggtgggaagc	agctaatacag	atcgcccagc	ctttggccct	2280

```

cagaaaaagt gctgaaacgt gcccttgac cggacgtcac agccctgcga gcattctgtg 2340
gactcaggcg tgctctttgc tggttcctgg gaggttggc cacatccctc atggcccat 2400
tttatcccg aaatcctggg tgtgtcacca gtgtagaggg tggggaaggg gtgtctcacc 2460
tgagctgact ttgttcttcc ttcacaacct tctgagcctt ctttgggatt ctggaaggaa 2520
ctcggcgtga gaaacatgtg acttcccctt tcccttccca ctgctgctt cccacagggc 2580
gacaggctgg gctggagaaa cagaaatcct caccctgcgt cttcccaagt tagcaggtgt 2640
ctctggtggt cagtgaggag gacatgtgag tcctggcaga agccatggcc catgtctgca 2700
catccaggga ggaggacaga aggccagct cacatgtgag tcctggcaga agccatggcc 2760
catgtctgca catccaggga ggaggacaga aggccagct cacatgtgag tcctggcaga 2820
agccatggcc catgtctgca catccaggga ggaggacaga aggccagct cacatgtgag 2880
tcctggcaga agccatggcc catgtctgca catccaggga ggaggacaga aggccagct 2940
cagtggcccc cgctccccac cccccacgcc cgaacagcag gggcagagca gccctccttc 3000
gaagtgtgtc caagtccgca tttagcctt gttctggggc ccagcccaac acctggcttg 3060
ggctcactgt cctgagttgc agtaaagcta taacctgaa tcacaa 3106

```

<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (539)

<223> Any amino acid

<400> 175

```

Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
  1                      5                      10                      15

Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
          20                      25                      30

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
          35                      40                      45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
          50                      55                      60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
          65                      70                      75                      80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
          85                      90                      95

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
          100                      105                      110

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
          115                      120                      125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
          130                      135                      140

```

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu
 145 150 155 160
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp
 165 170 175
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro
 180 185 190
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp
 195 200 205
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile
 210 215 220
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly
 225 230 235 240
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu
 245 250 255
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro
 260 265 270
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly
 275 280 285
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala
 290 295 300
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly
 305 310 315 320
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys
 325 330 335
 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly
 340 345 350
 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile
 355 360 365
 Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys Met Pro
 370 375 380
 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu
 385 390 395 400
 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu
 405 410 415
 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu
 420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His
435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp
450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val
465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn
485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp
500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser
515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr
530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr
545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val
565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln
580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln
595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr
610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys
625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

ggggacgcgg agctgagagg ctccgggcta gctaggtgta ggggtggacg ggtcccagga 60
ccctggtgag gggtctctac ttggccttcg gtgggggtca agacgcaggc acctacgcca 120
aaggggagca aagccgggct cggcccgagg cccccaggac ctccatctcc caatgttgga 180
ggaatccgac acgtgacggt ctgtccgccg tctcagacta gaggagcgct gtaaaccgcca 240
tggtcccaa gaagctgtcc tgccttcgtt cctgctgct gccgctcagc ctgacgctac 300
tgctgcccc ggcagacact cggtcgttcg tagtggatag gggtcatgac cggtttctcc 360
tagacggggc ccggttccgc tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420

tgctttgggc cgaccggctt ttgaagatgc gatggagcgg cctcaacgcc atacagtttt 480
 atgtgccctg gaactaccac gagccacagc ctgggggtcta taactttaat ggcagccggg 540
 acctcattgc ctttctgaat gaggcagctc tagcgaacct gttgggtcata ctgagaccag 600
 gaccttacat ctgtgcagag tgggagatgg ggggtctccc atcctgggtg cttcgaaaac 660
 ctgaaattca tctaagaacc tcagatccag acttccttgc cgcagtggac tcctgggttca 720
 aggtcttgcg gcccaagata tatccatggc tttatcacia tgggggcaac atcattagca 780
 ttcaggtgga gaatgaatat ggtagctaca gagcctgtga cttcagctac atgaggcact 840
 tggctgggct cttccgtgca ctgctaggag aaaagatctt gctcttcacc acagatgggc 900
 ctgaaggact caagtgtggc tccctccggg gactctatac cactgtagat tttggcccag 960
 ctgacaacat gaccaaatac tttaccctgc ttcggaagta tgaaccccat gggccattgg 1020
 taaactctga gtactacaca ggctggctgg attactgggg ccagaatcac tccacacggg 1080
 ctgtgtcagc tgtaaccaa ggactagaga acatgctcaa gttggggagc agtgtgaaca 1140
 tgtacatggt ccatggaggt accaactttg gatattggaa tgggtgccgat aagaagggac 1200
 gcttccttcc gattactacc agctatgact atgatgcacc tatatctgaa gcaggggacc 1260
 ccacacctaa gctttttgct cttcgagatg tcatcagcaa gttccaggaa gttccttttg 1320
 gacctttacc tccccgagc cccaagatga tgcttggacc tgtgactctg cacctgggtg 1380
 ggcatttact ggctttccta gacttgcttt gcccccggtg gccattcat tcaatcttgc 1440
 caatgacctt tgaggctgtc aagcaggacc atggcttcat gttgtaccga acctatatga 1500
 cccataccat ttttgagcca acaccattct ggggtgcaaa taatggagtc catgaccgtg 1560
 cctatgtgat ggtggatggg gtgttccagg gtgttgtgga gcgaaatatg agagacaaac 1620
 tatttttgac ggggaaactg ggggtccaaac tggatatctt ggtggagaac atggggaggc 1680
 tcagctttgg gtctaacagc agtgacttca agggcctgtt gaagccacca attctggggc 1740
 aaacaatcct taccagtggt atgatgttcc ctctgaaaat tgataacctt gtgaagtggg 1800
 ggtttccctt ccagttgcca aaatggccat atcctcaagc tccttctggc cccacattct 1860
 actccaaaac atttccaatt ttaggctcag ttggggacac atttctatat ctacctggat 1920
 ggaccaaggg ccaagtctgg atcaatgggt ttaacttggg ccggtactgg acaaagcagg 1980
 ggccacaaca gacctctac gtgccaagat tctgtctgtt tctagggga gccctcaaca 2040
 aaattacatt gctggaacta gaagatgtac ctctccagcc ccaagtccaa tttttggata 2100
 agcctatcct caatagcact agtactttgc acaggacaca tatcaattcc ctttcagctg 2160
 atacactgag tgccctctgaa ccaatggagt taagtgggca ctgaaaggta ggccgggcat 2220
 ggtggctcat gcctgtaatc ccagcacttt gggaggctga gacgggtgga ttacctgagg 2280
 tcaggacttc aagaccagcc tggccaacat ggtgaaaccc cgtctccact aaaaatacaa 2340
 aaattagccg ggcgtgatgg tgggcacctc taatcccagc tacttgggag gctgagggca 2400
 ggagaattgc ttgaatccag gaggcagagg ttgcagtgag tggaggttgt accactgcac 2460
 tccagcctgg ctgacagtga gacactccat ctcaaaaaaa aaaaa 2505

<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu
 1 5 10 15

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val
 20 25 30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
 35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
 50 55 60

Asp 65	Arg	Leu	Leu	Lys	Met 70	Arg	Trp	Ser	Gly	Leu 75	Asn	Ala	Ile	Gln	Phe 80
Tyr	Val	Pro	Trp	Asn 85	Tyr	His	Glu	Pro	Gln 90	Pro	Gly	Val	Tyr	Asn 95	Phe
Asn	Gly	Ser	Arg 100	Asp	Leu	Ile	Ala	Phe 105	Leu	Asn	Glu	Ala	Ala 110	Leu	Ala
Asn	Leu 115	Leu	Val	Ile	Leu	Arg	Pro 120	Gly	Pro	Tyr	Ile 125	Cys	Ala	Glu	Trp
Glu 130	Met	Gly	Gly	Leu	Pro	Ser 135	Trp	Leu	Leu	Arg	Lys 140	Pro	Glu	Ile	His
Leu 145	Arg	Thr	Ser	Asp 150	Pro	Asp	Phe	Leu	Ala 155	Ala	Val	Asp	Ser	Trp 160	Phe
Lys	Val	Leu	Leu 165	Pro	Lys	Ile	Tyr	Pro	Trp 170	Leu	Tyr	His	Asn 175	Gly	Gly
Asn	Ile	Ile	Ser 180	Ile	Gln	Val	Glu	Asn 185	Glu	Tyr	Gly	Ser	Tyr 190	Arg	Ala
Cys	Asp	Phe 195	Ser	Tyr	Met	Arg	His 200	Leu	Ala	Gly	Leu 205	Phe	Arg	Ala	Leu
Leu 210	Gly	Glu	Lys	Ile	Leu	Leu 215	Phe	Thr	Thr	Asp	Gly 220	Pro	Glu	Gly	Leu
Lys 225	Cys	Gly	Ser	Leu 230	Arg	Gly	Leu	Tyr	Thr 235	Thr	Val	Asp	Phe	Gly	Pro 240
Ala	Asp	Asn	Met 245	Thr	Lys	Ile	Phe	Thr 250	Leu	Leu	Arg	Lys	Tyr 255	Glu	Pro
His	Gly	Pro	Leu 260	Val	Asn	Ser	Glu	Tyr 265	Tyr	Thr	Gly	Trp	Leu 270	Asp	Tyr
Trp	Gly	Gln 275	Asn	His	Ser	Thr	Arg 280	Ser	Val	Ser	Ala 285	Val	Thr	Lys	Gly
Leu 290	Glu	Asn	Met	Leu	Lys	Leu 295	Gly	Ala	Ser	Val 300	Asn	Met	Tyr	Met	Phe
His 305	Gly	Gly	Thr	Asn 310	Phe	Gly	Tyr	Trp	Asn 315	Gly	Ala	Asp	Lys	Lys	Gly 320
Arg	Phe	Leu	Pro 325	Ile	Thr	Thr	Ser	Tyr 330	Asp	Tyr	Asp	Ala	Pro 335	Ile	Ser
Glu	Ala	Gly	Asp	Pro	Thr	Pro	Lys	Leu	Phe	Ala	Leu	Arg	Asp	Val	Ile

			340				345				350					
Ser	Lys	Phe	Gln	Glu	Val	Pro	Leu	Gly	Pro	Leu	Pro	Pro	Pro	Ser	Pro	
		355					360					365				
Lys	Met	Met	Leu	Gly	Pro	Val	Thr	Leu	His	Leu	Val	Gly	His	Leu	Leu	
		370				375					380					
Ala	Phe	Leu	Asp	Leu	Leu	Cys	Pro	Arg	Gly	Pro	Ile	His	Ser	Ile	Leu	
385					390					395						400
Pro	Met	Thr	Phe	Glu	Ala	Val	Lys	Gln	Asp	His	Gly	Phe	Met	Leu	Tyr	
				405					410					415		
Arg	Thr	Tyr	Met	Thr	His	Thr	Ile	Phe	Glu	Pro	Thr	Pro	Phe	Trp	Val	
			420					425					430			
Pro	Asn	Asn	Gly	Val	His	Asp	Arg	Ala	Tyr	Val	Met	Val	Asp	Gly	Val	
		435					440					445				
Phe	Gln	Gly	Val	Val	Glu	Arg	Asn	Met	Arg	Asp	Lys	Leu	Phe	Leu	Thr	
		450				455					460					
Gly	Lys	Leu	Gly	Ser	Lys	Leu	Asp	Ile	Leu	Val	Glu	Asn	Met	Gly	Arg	
465					470					475						480
Leu	Ser	Phe	Gly	Ser	Asn	Ser	Ser	Asp	Phe	Lys	Gly	Leu	Leu	Lys	Pro	
				485					490					495		
Pro	Ile	Leu	Gly	Gln	Thr	Ile	Leu	Thr	Gln	Trp	Met	Met	Phe	Pro	Leu	
			500					505					510			
Lys	Ile	Asp	Asn	Leu	Val	Lys	Trp	Trp	Phe	Pro	Leu	Gln	Leu	Pro	Lys	
		515					520					525				
Trp	Pro	Tyr	Pro	Gln	Ala	Pro	Ser	Gly	Pro	Thr	Phe	Tyr	Ser	Lys	Thr	
		530				535					540					
Phe	Pro	Ile	Leu	Gly	Ser	Val	Gly	Asp	Thr	Phe	Leu	Tyr	Leu	Pro	Gly	
545					550					555						560
Trp	Thr	Lys	Gly	Gln	Val	Trp	Ile	Asn	Gly	Phe	Asn	Leu	Gly	Arg	Tyr	
				565					570					575		
Trp	Thr	Lys	Gln	Gly	Pro	Gln	Gln	Thr	Leu	Tyr	Val	Pro	Arg	Phe	Leu	
			580					585					590			
Leu	Phe	Pro	Arg	Gly	Ala	Leu	Asn	Lys	Ile	Thr	Leu	Leu	Glu	Leu	Glu	
		595					600					605				
Asp	Val	Pro	Leu	Gln	Pro	Gln	Val	Gln	Phe	Leu	Asp	Lys	Pro	Ile	Leu	
		610				615					620					

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala
 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His
 645 650

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 178

tggtactcc aagaccctgg catg

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 179

tggacaaatc cccttgctca gccc

24

<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 180

gggcttcacc gaagcagtgg acctttatatt tgaccacctg atgtccaggg

50

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 181

ccagctatga ctatgatgca cc

22

TEF236TH260

<210> 182
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 182
 tggcaccag aatggtgtg gctc

24

<210> 183
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 183
 cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc

50

<210> 184
 <211> 1947
 <212> DNA
 <213> Homo sapiens

<400> 184
 gctttgaaca cgtctgcaag cccaaagttg agcatctgat tggttatgag gtatttgagt 60
 gcaccacaa tatggcttac atgttgaaaa agcttctcat cagttacata tccattattt 120
 gtgtttatgg ctttatctgc ctctacactc tcttctgggt attcaggata cctttgaagg 180
 aatattcttt cgaaaaagtc agagaagaga gcagtttttag tgacattcca gatgtcaaaa 240
 acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagcgtt 300
 ttggtgtgtt cttgtcagaa gttagtgaat ataaacttag ggaaattagt ttgaaccatg 360
 agtggacatt tgaaaaactc aggcagcaca ttacacgcaa cgcacaggac aagcaggagt 420
 tgcattctgt catgctgtcg ggggtgcccg atgctgtctt tgacctcaca gacctggatg 480
 tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540
 acctccaaga gctccacctc tgccactgcc ctgcaaaaagt tgaacagact gcttttagct 600
 ttcttcgcga tcacttgaga tgccttcacg tgaagttcac tgatgtggct gaaattcctg 660
 cctgggtgta tttgctcaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720
 aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780
 acgtgaagag caatttgacc aaagttccct ccaacattac agatgtggct ccacatctta 840
 caaagttagt cattcataat gacggcacta aactcttggt actgaacagc ctttaagaaa 900
 tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960
 ttttcagcct ctctaattta caggaactgg atttaaagtc caataacatt cgcacaattg 1020
 aggaaatcat cagttttccag catttaaaac gactgacttg tttaaaatta tggcataaca 1080
 aaattgttac tattctccc tctattacce atgtcaaaaa cttggagtca ctttatttct 1140
 ctaacaacaa gctcgaatcc ttaccagtgg cagtatttag tttacagaaa ctcatagct 1200
 tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattg cttcagaacc 1260
 tgcagcattt gcatatcact gggaacaaag tggacattct gccaaaacaa ttgttttaaa 1320

gcataaagtt gaggactttg aatctgggac agaactgcat cacctcactc ccagagaaaag 1380
 ttggtcagct ctcccagctc actcagctgg agctgaaggg gaactgcttg gaccgcctgc 1440
 cagcccagct gggccagtgt cggatgctca agaaaagcgg gcttggttg gaagatcacc 1500
 tttttgatac cctgccactc gaagtcaaag aggcattgaa tcaagacata aatattccct 1560
 ttgcaaagtg gatttaaact aagataatat atgcacagt atgtgcagga acaacttcct 1620
 agattgcaag tgctcacgta caagttatta caagataatg catttttagga gtagatacat 1680
 cttttaaaat aaaacagaga ggatgcatag aaggctgata gaagacataa ctgaatgttc 1740
 aatgtttgta gggttttaag tcattcattt ccaaattcatt tttttttttc ttttggggaa 1800
 aggggaaggaa aaattataat cactaatctt ggttcttttt aaattgtttg taacttggat 1860
 gctgccgcta ctgaatgttt acaaattgct tgcttgctaa agtaaattgat taaattgaca 1920
 ttttcttact aaaaaaaaaa aaaaaaa 1947

<210> 185

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile
 1 5 10 15

Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg
 20 25 30

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser
 35 40 45

Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His
 50 55 60

Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe
 65 70 75 80

Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His
 85 90 95

Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln
 100 105 110

Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala
 115 120 125

Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro
 130 135 140

Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu
 145 150 155 160

Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser
 165 170 175

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val
 180 185 190

TC001020.001


```
<400> 189
ccacgcgtc cggccttctc tctggacttt gcatttccat tccttttcat tgacaaactg 60
acttttttta tttctttttt tccatctctg ggccagcttg ggatcctagg ccgccttggg 120
aagacatttg tgttttacac acataaggat ctgtgttttg ggtttcttct tcctcccttg 180
```

acattggcat tgcttagtggt ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240
gcacttatct gcctaggtac atcgaagtct tttgacctcc atacagtgat tatgcctgtc 300
atcgctgggtg gtatcctggc ggccttgctc ctgctgatag ttgtcgtgct ctgtctttac 360
ttcaaaatac acaacgcgct aaaagctgca aaggaacctg aagctgtggc tgtaaaaaat 420
cacaacccag acaaggtgtg gtggggccaag aacagccagg ccaaaacccat tgccacggag 480
tcttgctcctg ccctgcagtg ctgtgaaggga tatagaatgt gtgccagttt tgattccctg 540
ccaccttgct gttgcgacat aaatgagggc ctctgagtta ggaaaggctc ctttctcaaa 600
gcagagccct gaagacttca atgatgtcaa tgaggccacc tgtttgtgat gtgcaggcac 660
agaagaaagg cacagctccc catcagtttc atggaaaata actcagtgcc tgctgggaac 720
cagctgctgg agatccctac agagagcttc cactgggggc aaccttcca ggaaggagt 780
ggggagagag aacctcact gtggggaatg ctgataaacc agtcacacag ctgctctatt 840
ctcacacaaa tctacccctt gcgtggctgg aactgacgtt tccctggagg tgtccagaaa 900
gctgatgtaa cacagagcct ataaaagctg tcggtcctta aggctgcca gcgccttgcc 960
aaaatggagc ttgtaagaag gctcatgcca ttgacctct taattctctc ctgtttggcg 1020
gagctgacaa tggcggaggc tgaaggcaat gcaagctgca cagtcagtct agggggtgcc 1080
aatatggcag agaccacaaa agccatgatc ctgcaactca atcccagtga gaactgcacc 1140
tggaacaatag aaagaccaga aaacaaaagc atcagaatta tcttttcta tgtccagctt 1200
gatccagatg gaagctgtga aagtgaaaac attaaagtct ttgacggaac ctccagcaat 1260
gggcctctgc tagggcaagt ctgcagtaaa aacgactatg ttctgtatt tgaatcatca 1320
tccagtacat tgacgtttca aatagtact gactcagcaa gaattcaaag aactgtcttt 1380
gtcttctact acttcttctc tctaaccatc tctattccaa actgtggcgg ttacctggat 1440
accttggaag gatccttcac cagccccaat tacccaaagc cgcacctga gctggcttat 1500
tgtgtgtggc acatacaagt ggagaaaagat tacaagataa aactaaactt caaagagatt 1560
ttcctagaaa tagacaaaca gtgcaaattt gattttcttg ccactatga tggccctcc 1620
accaactctg gcctgattgg acaagtctgt ggccgtgtga ctcccactt cgaatcgtca 1680
tcaaactctc tgactgtcgt gttgtctaca gattatgcca attcttaccg gggattttct 1740
gcttctaca cctcaattta tgcagaaaac atcaacacta catctttaac ttgctcttct 1800
gacaggatga gagttattat aagcaaatcc tacctagagg cttttaactc taatgggaat 1860
aacttgcaac taaaagaccc aacttgcaag ccaaaattat caaatgttgt ggaattttct 1920
gtccctctta atggatgtgg tacaatcaga aaggtagaag atcagtcaat tacttacacc 1980
aatataatca ctttttctgc atcctcaact tctgaagtga tcaccctca gaaacaactc 2040
cagattattg tgaagtgtga aatgggacat aattctacag tggagataat atacataaca 2100
gaagatgatg taatacaaaag tcaaaatgca ctgggcaaat ataacaccag catggctctt 2160
tttgaatcca attcatttga aaagactata cttgaatcac catattatgt ggatttgaac 2220
caaactcttt ttgttcaagt tagtctgcac acctcagatc caaatttggg ggtgtttctt 2280
gatactgtga gagcctctcc cacctctgac tttgcatctc caacctacga cctaatacaag 2340
agtggatgta gtcgagatga aacttgtaag gtgtatccct tatttggaca ctatgggaga 2400
ttccagttta atgcctttaa attcttgaga agtatgagct ctgtgtatct gcagtgtaaa 2460
gttttgatat gtgatagcag tgaccaccag tctcgtgca atcaagggtt tgtctccaga 2520
agcaaacgag acatttcttc atataaatgg aaaacagatt ccatcatagg acccattcgt 2580
ctgaaaagg atcgaagtgc aagtggcaat tcaggatttc agcatgaaac acatgcggaa 2640
gaaactcaa accagccttt caacagtgtg catctgtttt ccttcatggg tctagctctg 2700
aatgtggtga ctgtagcgac aatcacagtg aggcattttg taaatcaacg ggcagactac 2760
aaataccaga agctgcagaa ctattaacta acaggtccaa ccctaagtga gacatgtttc 2820
tccaggatgc caaaggaaat gctacctcgt ggctacacat attatgaata aatgaggaag 2880
ggcctgaaag tgacacacag gcctgcatgt aaaaaa 2917

<210> 190

<211> 607

<212> PRT

<213> Homo sapiens

<400> 190

Met 1	Glu	Leu	Val	Arg 5	Arg	Leu	Met	Pro	Leu 10	Thr	Leu	Leu	Ile	Leu 15	Ser
Cys	Leu	Ala	Glu 20	Leu	Thr	Met	Ala	Glu 25	Ala	Glu	Gly	Asn	Ala 30	Ser	Cys
Thr	Val	Ser 35	Leu	Gly	Gly	Ala	Asn 40	Met	Ala	Glu	Thr	His 45	Lys	Ala	Met
Ile 50	Leu	Gln	Leu	Asn	Pro 55	Ser	Glu	Asn	Cys	Thr	Trp 60	Thr	Ile	Glu	Arg
Pro 65	Glu	Asn	Lys	Ser 70	Ile	Arg	Ile	Ile	Phe	Ser 75	Tyr	Val	Gln	Leu	Asp 80
Pro	Asp	Gly	Ser 85	Cys	Glu	Ser	Glu	Asn 90	Ile	Lys	Val	Phe	Asp 95	Gly	Thr
Ser	Ser	Asn 100	Gly	Pro	Leu	Leu	Gly	Gln 105	Val	Cys	Ser	Lys	Asn 110	Asp	Tyr
Val	Pro 115	Val	Phe	Glu	Ser	Ser	Ser 120	Ser	Thr	Leu	Thr	Phe 125	Gln	Ile	Val
Thr 130	Asp	Ser	Ala	Arg	Ile 135	Gln	Arg	Thr	Val	Phe 140	Val	Phe	Tyr	Tyr	Phe
Phe 145	Ser	Pro	Asn	Ile 150	Ser	Ile	Pro	Asn	Cys	Gly 155	Gly	Tyr	Leu	Asp	Thr 160
Leu	Glu	Gly	Ser 165	Phe	Thr	Ser	Pro	Asn	Tyr 170	Pro	Lys	Pro	His	Pro	Glu
Leu	Ala	Tyr 180	Cys	Val	Trp	His	Ile 185	Gln	Val	Glu	Lys	Asp	Tyr 190	Lys	Ile
Lys	Leu 195	Asn	Phe	Lys	Glu	Ile 200	Phe	Leu	Glu	Ile	Asp	Lys 205	Gln	Cys	Lys
Phe 210	Asp	Phe	Leu	Ala	Ile 215	Tyr	Asp	Gly	Pro	Ser	Thr 220	Asn	Ser	Gly	Leu
Ile 225	Gly	Gln	Val	Cys 230	Gly	Arg	Val	Thr	Pro	Thr 235	Phe	Glu	Ser	Ser	Ser
Asn	Ser	Leu	Thr 245	Val	Val	Leu	Ser	Thr	Asp 250	Tyr	Ala	Asn	Ser 255	Tyr	Arg
Gly	Phe	Ser 260	Ala	Ser	Tyr	Thr	Ser	Ile 265	Tyr	Ala	Glu	Asn	Ile 270	Asn	Thr
Thr	Ser 275	Leu	Thr	Cys	Ser	Ser	Asp 280	Arg	Met	Arg	Val	Ile 285	Ile	Ser	Lys

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys
 290 295 300
 Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val
 305 310 315 320
 Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile
 325 330 335
 Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val
 340 345 350
 Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly
 355 360 365
 His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile
 370 375 380
 Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe
 385 390 395 400
 Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val
 405 410 415
 Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp
 420 425 430
 Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser
 435 440 445
 Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg
 450 455 460
 Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe
 465 470 475 480
 Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu
 485 490 495
 Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys
 500 505 510
 Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys
 515 520 525
 Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg
 530 535 540
 Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu
 545 550 555 560
 Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

	565	570	575
Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe			
580	585	590	
Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr			
595	600	605	

<210> 191
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 191
 tctctattcc aaactgtggc g 21

<210> 192
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 192
 tttgatgacg attcgaaggt gg 22

<210> 193
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 193
 ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc 47

<210> 194
 <211> 2362
 <212> DNA
 <213> Homo sapiens

<400> 194
 gacggaagaa cagcgctccc gaggccgcgg gagcctgcag agaggacagc cggcctgcgc 60
 cgggacatgc ggccccagga gctccccagg ctgcggttcc cggtgctgct gttgctgttg 120
 ctgctgctgc cgccgcgcgc gtgccctgcc cacagcgcca cgcgcttcga cccacctgg 180


```

gagtcacctg acgcccccca gctgcccgcg tggtttgacc aggccaaagt cggcatcttc 240
atccactggg gagtggtttc cgtgcccagc ttcggtagcg agtggttctg gtggtatttg 300
caaaaggaaa agataccgaa gtatgtggaa tttatgaaag ataattacc ccttagtttc 360
aaatatgaag attttggacc actatttaca gcaaaatttt ttaatgccaa ccagtgggca 420
gatatttttc aggcctctgg tgccaaatac attgtcttaa cttccaaaca tcatgaaggc 480
tttaccttgt ggggggtcaga atattcgtgg aactggaatg ccatagatga gggggccaaag 540
agggacattg tcaaggaaact tgaggtagcc attaggaaca gaactgacct gcgttttggg 600
ctgtactatt ccctttttga atggtttcat ccgctcttcc ttgaggatga atccagttca 660
ttccataagc ggcaatttcc agtttctaag acattgccag agctctatga gttagtgaac 720
aactatcagc ctgaggttct gtggtcggat ggtgacggag gagcaccgga tcaatactgg 780
aacagcacag gcttcttggc ctggttatat aatgaaagcc cagttcgggg cacagtagtc 840
accaatgatc gttggggagc tggtagcatc tgtaagcatg gtggcttcta tacctgcagt 900
gatcgttata acccaggaca tcttttgcca cataaatggg aaaactgcat gacaatagac 960
aaactgtcct ggggctatag gagggaaagt ggaatctctg actatcttac aattgaagaa 1020
ttggtgaagc aacttgtaga gacagtttca tgtggaggaa atcttttgat gaattattggg 1080
cccacactag atggcaccat ttctgtagtt tttgaggagc gactgaggca agtgggggtcc 1140
tggtctaaaag tcaatggaga agctatttat gaaacctata cctggcgatc ccagaatgac 1200
actgtcacc cagatgtgtg gtacacatcc aagcctaaag aaaaattagt ctatgccatt 1260
tttcttaaat ggcccacatc aggacagctg ttccttggcc atcccaaagc tattctgggg 1320
gcaacagagg tgaaactact gggccatgga cagccactta actggatttc ttggagcaa 1380
aatggcatta tggtagaact gccacagcta accattcatc agatgccgtg taaatggggc 1440
tgggctctag ccctaactaa tgtgatctaa agtgcagcag agtggctgat gctgcaagtt 1500
atgtctaagg ctaggaacta tcaggtgtct ataattgtag cacatggaga aagcaatgta 1560
aactggataa gaaaattatt tggcagttca gccctttccc tttttccac taaatttttc 1620
ttaaattacc catgtaacca ttttaactct ccagtgcact ttgccattaa agtctcttca 1680
cattgatttg tttccatgtg tgactcagag gtgagaattt tttcacatta tagtagcaag 1740
gaattgggtg tattatggac cgaactgaaa attttatgtt gaagccatat ccccatgat 1800
tatatagtta tgcatactt aatatgggga tttttctggt gaaatgcatt gctagtcaat 1860
ttttttttgt gccaacatca tagagtgtat ttacaaaatc ctagatggca tagcctacta 1920
cacaccta at gtgtatggta tagactgttg ctcttaggct acagacatat acagcatgtt 1980
actgaatact gtaggcaata gtaacagtgg tatttgtata tcgaaacata tggaaacata 2040
gagaaggtag agtaaaaata ctgtaaaata aatggtgcac ctgtataggg cacttaccac 2100
gaatggagct tacaggactg gaagttgtct tgggtgagtc agtgagtga tgtgaaggcc 2160
taggacatta ttgaacactg ccagacgtta taaatactgt atgcttaggc tacactacat 2220
ttataaaaaa aagtttttct ttcttcaatt ataaattaac ataagtgtac tgtaacttta 2280
caaacgtttt aatttttaaa acctttttgg ctcttttgta ataactta gcttaaaaca 2340
taaactcatt gtgcaaatgt aa 2362

```

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu
1 5 10 15

Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr
20 25 30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
35 40 45

Trp	Phe	Asp	Gln	Ala	Lys	Phe	Gly	Ile	Phe	Ile	His	Trp	Gly	Val	Phe
50						55				60					
Ser	Val	Pro	Ser	Phe	Gly	Ser	Glu	Trp	Phe	Trp	Trp	Tyr	Trp	Gln	Lys
65					70					75					80
Glu	Lys	Ile	Pro	Lys	Tyr	Val	Glu	Phe	Met	Lys	Asp	Asn	Tyr	Pro	Pro
				85					90					95	
Ser	Phe	Lys	Tyr	Glu	Asp	Phe	Gly	Pro	Leu	Phe	Thr	Ala	Lys	Phe	Phe
			100					105					110		
Asn	Ala	Asn	Gln	Trp	Ala	Asp	Ile	Phe	Gln	Ala	Ser	Gly	Ala	Lys	Tyr
		115					120					125			
Ile	Val	Leu	Thr	Ser	Lys	His	His	Glu	Gly	Phe	Thr	Leu	Trp	Gly	Ser
	130					135					140				
Glu	Tyr	Ser	Trp	Asn	Trp	Asn	Ala	Ile	Asp	Glu	Gly	Pro	Lys	Arg	Asp
145					150					155					160
Ile	Val	Lys	Glu	Leu	Glu	Val	Ala	Ile	Arg	Asn	Arg	Thr	Asp	Leu	Arg
				165					170					175	
Phe	Gly	Leu	Tyr	Tyr	Ser	Leu	Phe	Glu	Trp	Phe	His	Pro	Leu	Phe	Leu
			180					185					190		
Glu	Asp	Glu	Ser	Ser	Ser	Phe	His	Lys	Arg	Gln	Phe	Pro	Val	Ser	Lys
		195					200					205			
Thr	Leu	Pro	Glu	Leu	Tyr	Glu	Leu	Val	Asn	Asn	Tyr	Gln	Pro	Glu	Val
	210					215					220				
Leu	Trp	Ser	Asp	Gly	Asp	Gly	Gly	Ala	Pro	Asp	Gln	Tyr	Trp	Asn	Ser
225					230					235					240
Thr	Gly	Phe	Leu	Ala	Trp	Leu	Tyr	Asn	Glu	Ser	Pro	Val	Arg	Gly	Thr
				245					250					255	
Val	Val	Thr	Asn	Asp	Arg	Trp	Gly	Ala	Gly	Ser	Ile	Cys	Lys	His	Gly
			260					265					270		
Gly	Phe	Tyr	Thr	Cys	Ser	Asp	Arg	Tyr	Asn	Pro	Gly	His	Leu	Leu	Pro
		275					280					285			
His	Lys	Trp	Glu	Asn	Cys	Met	Thr	Ile	Asp	Lys	Leu	Ser	Trp	Gly	Tyr
	290					295					300				
Arg	Arg	Glu	Ala	Gly	Ile	Ser	Asp	Tyr	Leu	Thr	Ile	Glu	Glu	Leu	Val
305					310					315					320
Lys	Gln	Leu	Val	Glu	Thr	Val	Ser	Cys	Gly	Gly	Asn	Leu	Leu	Met	Asn
				325					330					335	

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg
 340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr
 355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val
 370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu
 385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
 405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn
 420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu
 435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr
 450 455 460

Asn Val Ile
 465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 196

tggtttgacc aggccaaagt cgg

23

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 197

ggattcatcc tcaaggaaga gcgg

24

<210> 198

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 198

aacttgcagc atcagccact ctgc

24

<210> 199

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 199

ttccgtgcc agcttcggta gcgagtgggt ctggtgggtat tggca

45

<210> 200

<211> 2372

<212> DNA

<213> Homo sapiens

<400> 200

```

agcagggaaa tccggatgtc tcggttatga agtggagcag tgagtgtgag cctcaacata 60
gttccagaac tctccatccg gactagttat tgagcatctg cctctcatat caccagtggc 120
catctgaggt gtttcccttg ctctgaagggt gtaggcacga tggccagggtg cttcagcctg 180
gtgttgcttc tcacttccat ctggaccacg aggtcctctg tccaaggctc ttgctgtgca 240
gaagaagctt ccactcaggt gtcattgcaga attatgggga tcacccttgt gagcaaaaag 300
gcgaaccagc agctgaattt cacagaagct aaggaggcct gtaggctgct gggactaagt 360
ttggccggca aggaccaagt tgaaacagcc ttgaaagcta gctttgaaac ttgcagctat 420
ggctgggttg gagatggatt cgtgggtcatc tctaggatta gcccaaacc caagtgtggg 480
aaaaatgggg tgggtgtcct gatttggaag gttccagtga gccgacagtt tgcagcctat 540
tgttacaact catctgatac ttggactaac tcgtgcattc cagaaattat caccaccaa 600
gatcccatat tcaacactca aactgcaaca caaacaacag aatttattgt cagtgcagct 660
acctactcgg tggcatcccc ttactctaca atacctgcc ctactactac tctcctgct 720
ccagcttcca cttctattcc acggagaaaa aaattgattt gtgtcacaga agtttttatg 780
gaaactagca ccatgtctac agaaactgaa ccatttggtg aaaataaagc agcattcaag 840
aatgaagctg ctgggttttg aggtgtcccc acggctctgc tagtgcttgc tctcctcttc 900
tttgggtgct cagctgggtc tggattttgc tatgtcaaaa ggtatgtgaa ggccttccct 960
tttacaacaa agaatcagca gaaggaaatg atcgaaacca aagtagtaaa ggaggagaag 1020
gccaatgata gcaaccctaa tgaggaatca aagaaaactg ataaaaacc agaagagtcc 1080
aagagtccaa gcaaaactac cgtgcgatgc ctggaagctg aagtttagat gagacagaaa 1140
tgaggagaca cacctgaggtc tggtttcttt catgctcctt accctgcccc agctggggaa 1200
atcaaaaggc ccaaagaacc aaagaagaaa gtccaccctt ggttcctaac tggaaatcagc 1260
tcaggactgc cattggacta tggagtgcac caaagagaat gcccttctcc ttattgtaac 1320
cctgtctgga tctatctc ctacctcaa agcttccac gcccttctta gcctggctat 1380
gtcctaataa tatccactg ggagaaagga gttttgcaaa gtgcaaggac ctaaaacatc 1440

```


Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr
 145 150 155 160
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser
 165 170 175
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser
 180 185 190
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu
 195 200 205
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala
 210 215 220
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu
 225 230 235 240
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe
 245 250 255
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn
 260 265 270
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala
 275 280 285
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro
 290 295 300
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala
 305 310 315 320
 Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 202

gagctttcca tccaggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

gtcagtgaca gtacctactc gg

22

<211> 24

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

tggagcagga ggagtagtag tagg

24

<211> 50

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt

50

<211> 1620

<212> DNA

<213> Homo sapiens

<221> modified base

<222> (973)

<223> a, t, c or g

<221> modified base

<222> (977)

<223> a, t, c or g

<221> modified_base

<222> (996)

<223> a, t, c or g

<221> modified base

<222> (1003)

<223> a, t, c or g

<400> 206

```

agatggcggg cttggcacct ctaattgctc tcgtgtattc ggtgccgcga ctttcacgat 60
ggctcgccca accttactac cttctgtcgg ccctgctctc tgctgccttc ctactcgtga 120
ggaaactgcc gccgctctgc cacggtctgc ccaccaacg cgaagacggg aaccctgtgt 180
actttgactg gagagaagtg gagatcctga tgtttctcag tgccattgtg atgatgaaga 240
accgcagatc catcactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300
ccaacacaat tcttttcttc cgcttgataa ttgcgatggg cctactttac atcacactct 360
gcatagtgtt cctgatgacg tgcaaaccce ccctatatat gggccctgag tatatcaagt 420
acttcaatga taaaaccatt gatgaggaac tagaacggga caagaggggc acttggattg 480
tggagtctct tgccaattgg tctaattgact gccaatcatt tgcccttacc tatgctgacc 540
tctcccttaa atacaactgt acagggctaa attttgggaa ggtggatgtt ggacgctata 600
ctgatgttag tacgcgggtac aaagttagca catcacccct caccaagcaa ctccctaccc 660
tgatcctgtt ccaaggtggc aaggaggcaa tgccggcgcc acagattgac aagaaaggac 720
gggctgtctc atggaccttc tctgaggaga atgtgatccg agaatttaac ttaaattgagc 780
tataccagcg ggccaagaaa ctatcaaagg ctggagacaa tatccctgag gacgagcctg 840
tggcttcaac ccccaccaca gtgtcagatg gggaaaacaa gaaggataaa taagatcctc 900
actttggcag tgcttctctc cctgtcaatt ccaggctctt tccataacca caagcctgag 960
gctgcagcct ttnattnatg ttttcccttt ggctgngact ggntggggca gcatgcagct 1020
tctgatttta aagaggcatc tagggaattg tcaggcaccc tacaggaagg cctgccatgc 1080
tgtggccaac tgtttactcgt gagcaagaaa gagatctcat aggacggagg gggaaatggg 1140
ttccctccaa gcttgggtca gtgtgttaac tgcttatcag ctattcagac atctccatgg 1200
tttctccatg aaactctgtg gtttcatcat tccttcttag ttgacctgca cagcttgggt 1260
agacctagat ttaaccctaa ggtaagatgc tggggtatag aacgctaaga attttcccc 1320
aaggactctt gcttccctaa gcccttctgg ctctgtttat ggtcttcatt aaaagtataa 1380
gcctaacttt gtcgctagtc ctaaggagaa acctttaacc acaaagtttt tatcattgaa 1440
gacaatattg aacaaccccc tattttgtgg ggattgagaa ggggtgaata gaggcttgag 1500
actttccttt gtgtggtagg acttggagga gaaatcccc ggactttcac taacctctctg 1560
acatactccc cacaccaggt tgatggcttt ccgtaataaa aagattggga tttccttttg 1620

```

<210> 207

<211> 296

<212> PRT

<213> Homo sapiens

<400> 207

```

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
  1              5              10              15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
  20              25              30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
  35              40              45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
  50              55              60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
  65              70              75              80

```



```
<210> 208
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 208
gcttgatat tcgcatgggc ctac
```

<210> 209
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 209
 tggagacaat atccctgagg 20

<210> 210
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 210
 aacagttggc cacagcatgg cagg 24

<210> 211
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 211
 ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212
 <211> 1985
 <212> DNA
 <213> Homo sapiens

<400> 212
 ggacagctcg cggcccccca gagctctagc cgtcgaggag ctgcctgggg acgtttgccc 60
 tggggcccca gcctggcccg ggtcaccctg gcatgaggag atgggcctgt tgctcctggt 120
 cccattgtct ctgctgccc gctcctacgg actgcccttc tacaacggct tctactactc 180
 caacagcgcc aacgaccaga acctaggcaa cggcatggc aaagacctcc ttaatggagt 240
 gaagctggtg gtggagacac ccgaggagac cctgttcacc taccaagggg ccagtgtgat 300
 cctgccttgc cgtaccgct acgagccggc cctgggtctcc ccgcggcgtg tgcgtgtcaa 360
 atggtggaag ctgtcggaga acggggcccc agagaaggac gtgctggtgg ccatcgggct 420
 gaggcacgcg tcctttgggg actaccaagg ccgcgtgcac ctgcggcagg acaaagagca 480
 tgacgtctcg ctggagatcc aggatctgcg gctggaggac tatgggctgt accgctgtga 540
 ggtcattgac gggctggagg atgaaagcgg tctggtggag ctggagctgc ggggtgtggt 600

```

ctttccttac cagtccccca acgggcgcta ccagttcaac ttccacgagg gccagcaggt 660
ctgtgcagag caggctgcgg tgggtggcctc ctttgagcag ctcttcgagg cctgggagga 720
gggcctggac tgggtgcaac cgggctggct gcaggatgct acggtgcagt accccatcat 780
gttgccccgg cagccctgcg gtggcccagg cctggcacct ggcgtgcgaa gctacggccc 840
ccgccaccgc cgctgcacc gctatgatgt attctgcttc gctactgcc tcaaggggcg 900
ggtgtactac ctggagcacc ctgagaagct gacgtgcaca gaggcaaggg aggcctgcca 960
ggaagatgat gccacgatcg ccaaggtggg acagctcttt gccgcctgga agttccatgg 1020
cctggaccgc tgcgacgtg gctggctggc agatggcagc gtccgtacc ctgtggttca 1080
cccgcatcct aactgtgggc cccagagacc tggggtccga agctttggct tccccgacc 1140
gcagagccgc ttgtacggtg tttactgcta ccgccagcac taggacctgg ggcctcccc 1200
tgccgcattc cctcactggc tgtgtattta ttgagtgggt cgttttccct tgtgggttgg 1260
agccatttta actgttttta tacttctcaa tttaaatttt ctttaaacad ttttttacta 1320
ttttttgtaa agcaaacaga acccaatgcc tcoctttgct cctggatgcc cactccagg 1380
aatcatgctt gctccccctg gccatttgcg gttttgtggg cttctggagg gttccccgcc 1440
atccaggtcg gtctccctcc cttaaggagg ttggtgccc gagtgggagg tggcctgtct 1500
agaatgccgc cgggagtcg ggcattggtg gcacagttct ccctgcccct cagcctgggg 1560
gaagaagagg gcctcggggg cctccggagc tgggctttgg gcctctctg cccacctcta 1620
cttctctgtg aagccgctga cccagtcctg cccactgagg ggctagggct ggaagccagt 1680
tctaggcttc caggcgaat ctgagggaag gaagaaactc cctcccccgt tcccttccc 1740
ctctcggttc caaagaatct gttttgtgt catttgttc tctgtttcc ctgtgtgggg 1800
agggggcctc aggtgtgtgt actttggaca ataaatggtg ctatgactgc cttccgccc 1860
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
aaaaaa                                           1985

```

<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

```

Met Gly Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr
  1             5             10            15

```

```

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
      20             25             30

```

```

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
      35             40             45

```

```

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
      50             55             60

```

```

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
      65             70             75            80

```

```

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
      85             90            95

```

```

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe
     100            105            110

```

```

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

```

115	120	125
Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr 130 135 140		
Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu 145 150 155 160		
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg 165 170 175		
Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala 180 185 190		
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly 195 200 205		
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr 210 215 220		
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro 225 230 235 240		
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp 245 250 255		
Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu 260 265 270		
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu 275 280 285		
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys 290 295 300		
Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser 305 310 315 320		
Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu 325 330 335		
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr 340 345 350		
Gly Val Tyr Cys Tyr Arg Gln His 355 360		

<210> 214

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 214

tgcttcgcta ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 215

ttcccttggtg ggttggag

18

<210> 216

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 216

agggctggaa gccagttc

18

<210> 217

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 217

agccagtggag gaaatgcg

18

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 218

tgtccaaagt acacacacct gagg

24

129

<210> 219

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 219

gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag

45

<210> 220

<211> 1503

<212> DNA

<213> Homo sapiens

<400> 220

```

ggagagcgga gcgaagctgg ataacagggg accgatgatg tggcgacat cagttctgct 60
gcttctgttg ctactgaggc acggggccca ggggaagcca tcccagacg caggccctca 120
tgccagggg aggggtgcacc aggcggcccc cctgagcgac gctcccatg atgacgcca 180
cgggaacttc cagtacgacc atgaggtttt cctgggacgg gaagtggcca aggaattcga 240
ccaactcacc ccagaggaaa gccaggcccc tctggggcgg atcgtggacc gcatggaccg 300
cgcgggggac ggcgacggct ggggtgtcgt ggcgagctt cgcgcgtgga tcgcgcacac 360
gcagcagcgg cacatacggg actcgggtgag cgcggcctgg gacacgtacg acacggaccg 420
cgacgggcgt gtgggttggg aggagctgcg caacgccacc tatggccact acgcgcccgg 480
tgaagaattt catgacgtgg aggatgcaga gacctacaaa aagatgctgg ctcgggacga 540
gcggcgtttc cgggtggccg accaggatgg ggactcgatg gccactcgag aggagctgac 600
agccttcctg caccgcgagg agttccctca catgcgggac atcgtgattg ctgaaaccct 660
ggaggacctg gacagaaaca aagatggcta tgtccagggt gaggagtaca tcgcggatct 720
gtactcagcc gagcctgggg aggaggagcc ggcgtgggtg cagacggaga ggcagcagtt 780
ccgggacttc cgggatctga acaaggatgg gcacctggat gggagtgagg tgggccactg 840
ggtgctgccc cctgcccagg accagccctt ggtggaagcc aaccacctgc tgcacgagag 900
cgacacggac aaggatgggc ggctgagcaa agcggaaatc ctgggtaatt ggaacatgtt 960
tgtgggcagt caggccacca actatggcga ggacctgacc cggcaccacg atgagctgtg 1020
agcaccgcgc acctgccaca gcctcagagg ccgcacaaat gaccggagga ggggcccgtg 1080
tggtctggcc cctcctctgt ccaggccccg caggaggcag atgcagtccc aggcatactc 1140
ctgcccctgg gctctcaggg accccttggg tcggcttctg tcctgtcac accccaacc 1200
ccagggaggg gctgtcatag tcccagagga taagcaatac ctatttctga ctgagtctcc 1260
cagcccagac ccagggaccc ttggcccca gctcagctct aagaaccgcc ccaaccctc 1320
cagctccaaa tctgagctc caccacatag actgaaactc ccctggcccc agccctctcc 1380
tgcttggcct ggcctgggac acctcctctc tgccaggagg caataaaagc cagcgcgggg 1440
accttgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
aaa 1503

```

<210> 221

<211> 328

<212> PRT

<213> Homo sapiens

<400> 221

Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 225
 cccccctgag cgacgctccc ccatgatgac gccacgga actt

44

<210> 226
 <211> 2403
 <212> DNA
 <213> Homo sapiens

<400> 226
 ggggccttgc cttccgcact cgggcgcage cgggtggatc tgcagcaggt gcggagcccc 60
 gggcggcggg cgcgggtgcg agggatccct gacgcctctg tccctgtttc tttgtcgctc 120
 ccagcctgtc tgtcgtcggt ttggcgcccc cgcctccccg cgggtgcgggg ttgcacaccg 180
 atcctgggct tgcctcgatt tgccgcgcag gcgcctccca gacctagagg ggcgtggcc 240
 tggagcagcg ggtcgtctgt gtccctctctc ctctgcgcgc cgcgcgggga tccgaagggt 300
 gcggggctct gaggaggtga cgcgcggggc ctccgcacc ctggccttgc ccgcattctc 360
 cctctctccc aggtgtgagc agcctatcag tcaccatgtc cgcagcctgg atcccggtc 420
 tcggcctcgg tgtgtgtctg ctgctgctgc cggggccccg gggcagcag ggagccgctc 480
 ccattgctat cacatgtttt accagaggct tggacatcag gaaagagaaa gcagatgtcc 540
 tctgcccagg gggctgccct cttgaggaat tctctgtgta tgggaacata gtatatgctt 600
 ctgtatcgag catatgtggg gctgctgtcc acaggggagt aatcagcaac tcagggggac 660
 ctgtacgagt ctatagccta cctggtcgag aaaactattc ctcagtagat gccaatggca 720
 tccagtctca aatgctttct agatggctctg cttctttcac agtaactaaa ggcaaaagta 780
 gtacacagga gggcacagga caagcagtgt ccacagcaca tccaccaaca ggtaaacgac 840
 taaagaaaac acccgagaag aaaactggca ataaagattg taaagcagac attgcatttc 900
 tgattgatgg aagctttaat attgggcagc gccgatttaa tttacagaag aattttgttg 960
 gaaaagtggc tctaattgtt ggaattggaa cagaaggacc acatgtgggc cttgttcaag 1020
 ccagtgaaca tcccaaaata gaattttact tgaaaaactt tacatcagcc aaagatgttt 1080
 tgtttgccat aaaggaagta gggttcagag ggggtaatc caatacagga aaagccttga 1140
 agcatactgc tcagaaattc ttacggtag atgctggagt aagaaaagg atcccaaaag 1200
 tgggtgggtg atttattgat gggtggcctt ctgatgacat cgaggaagca ggcattgttg 1260
 ccagagagtt tgggtgtcaat gtatttatag tttctgtggc caagcctatc cctgaagaac 1320
 tggggatggt tcaggatgtc acatttgttg acaaggctgt ctgtcggaat aatggcttct 1380
 tctcttacca catgcccac tgggttggca ccacaaaata cgtaaagcct ctgggtacaga 1440
 agctgtgcac tcatgaacaa atgatgtgca gcaagacctg ttataactca gtgaacattg 1500
 cctttctaat tgatggctcc agcagtgttg gagatagcaa tttccgcctc atgcttgaat 1560
 ttgtttccaa catagccaag acttttgaaa tctcggacat tggtgccaag atagctgctg 1620
 tacagtttac ttatgatcag cgcacggagt tcagtttcac tgactatagc accaaagaga 1680
 atgtcctagc tgtcatcaga aacatccgct atatgagtgg tggacagct actggtgatg 1740
 ccatttcctt cactgttaga aatgtgtttg gccctataag ggagagcccc aacaagaact 1800
 tcttagtaat tgtcacagat gggcagtcct atgatgatgt ccaaggccct gcagctgctg 1860
 cacatgatgc aggaatcact atcttctctg ttggtgtggc ttgggcacct ctggatgacc 1920
 tgaaagatat ggcttctaaa ccgaaggagt ctacgcctt cttcacaaga gagttcacag 1980
 gattagaacc aattgtttct gatgtcatca gaggcatttg tagagatttc ttagaatccc 2040
 agcaataatg gtaacathtt gacaactgaa agaaaaagta caaggggatc cagtgtgtaa 2100
 attgtattct cataatactg aaatgcttta gcatactaga atcagatata aaactattaa 2160
 gtatgtcaac agccatttag gcaaataagc actcctttaa agccgctgcc ttctggttac 2220
 aatttacagt gtactttgtt aaaaacactg ctgaggcttc ataactatgg ctcttagaaa 2280
 ctgaggaaag aggagataat gtggattaaa accttaagag ttctaaccat gctactaaa 2340
 tgtacagata tgcaaatcc atagctcaat aaaagaatct gatacttaga ccaaaaaaaaa 2400
 aaa 2403

<210> 227

<211> 550

<212> PRT

<213> Homo sapiens

<400> 227

Met Ser Ala Ala Trp Ile Pro Ala Leu Gly Leu Gly Val Cys Leu Leu
 1 5 10 15

Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile
 20 25 30

Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val
 35 40 45

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn
 50 55 60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg
 65 70 75 80

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro
 85 90 95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln
 100 105 110

Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser
 115 120 125

Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro
 130 135 140

Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys
 145 150 155 160

Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile
 165 170 175

Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala
 180 185 190

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln
 195 200 205

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser
 210 215 220

Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly
 225 230 235 240

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe
 245 250 255

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val
 260 265 270
 Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val
 275 280 285
 Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro
 290 295 300
 Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys
 305 310 315 320
 Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp
 325 330 335
 Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr
 340 345 350
 His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile
 355 360 365
 Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg
 370 375 380
 Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser
 385 390 395 400
 Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg
 405 410 415
 Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala
 420 425 430
 Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp
 435 440 445
 Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser
 450 455 460
 Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp
 465 470 475 480
 Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile
 485 490 495
 Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met
 500 505 510
 Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr
 515 520 525
 Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp
 530 535 540

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

<211> 18
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 232

ttcctcaaga gggcagcc

18

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 233

cttggcacca atgtccgaga tttc

24

<210> 234

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 234

gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg

45

<210> 235

<211> 2586

<212> DNA

<213> Homo sapiens

<400> 235

cgccgcgctc ccgcacccgc ggcccgccca ccgcgcgct cccgcatctg caccgcgagc 60
 ccggcggcct cccggcgagg ggcagcagat ccagtccggc ccgcagcgca actcgggtcca 120
 gtcggggcgg cggtgcggg cgcagagcgg agatgcagcg gcttggggcc accctgctgt 180
 gcctgctgct ggccggcgcc gtccccacgg ccccgcgccc cgctccgacg gcgacctcgg 240
 ctccagtc aa gcccggccc gctctcagct acccgcgagga ggaggccacc ctcaatgaga 300
 tggtccgcga ggttgaggaa ctgatggagg acacgcagca caaattgcgc agcgcggtgg 360
 aagagatgga ggcagaagaa gctgctgcta aagcatcatc agaagtgaac ctggcaaaact 420
 tacctcccag ctatcacaat gagaccaaca cagacacgaa ggttggaat aataccatcc 480
 atgtgcaccg agaaattcac aagataacca acaaccagac tggacaaatg gtcttttcag 540
 agacagttat cacatctgtg ggagacgaag aaggcagaag gagccacgag tgcacatcag 600
 acgaggactg tggggccagc atgtactgcc agtttgccag cttccagtac acctgccagc 660
 catgccgggg ccagaggatg ctctgcaccc gggacagtga gtgctgtgga gaccagctgt 720

gtgtctgggg tcaactgcacc aaaatggcca ccaggggcag caatgggacc atctgtgaca 780
 accagagggga ctgccagccg gggctgtgct gtgccttcca gagaggcctg ctgttccctg 840
 tgtgcacacc cctgcccgtg gagggcgagc ttgccatga ccccgccagc cggcttcttg 900
 acctcatcac ctgggagcta gagcctgatg gagccttggg cccgatgccct tgtgccagt 960
 gcctcctctg ccagccccac agccacagcc tgggtgtatgt gtgcaagccg accttcgtgg 1020
 ggagccgtga ccaagatggg gagatcctgc tgcccagaga ggtccccgat gaggatgaag 1080
 ttggcagctt catggaggag gtgcgccagg agctggagga cctggagagg agcctgactg 1140
 aagagatggc gctgggggag cctgcggctg ccgcgctgc actgctggga ggggaagaga 1200
 tttagatctg gaccaggctg tgggtagatg tgcaatagaa atagctaatt tatttcccca 1260
 ggtgtgtgct ttaggcgtgg gctgaccagg cttcttccca catcttcttc ccagtaagtt 1320
 tccccctctg cttgacagca tgaggtgttg tgcatttggt cagctcccc aggtctgttct 1380
 ccaggcttca cagtctggtg cttgggagag tcaggcaggg ttaaactgca ggagcagttt 1440
 gccacccctg tccagattat tggctgcttt gcctctacca gttggcagac agccgtttgt 1500
 tctacatggc tttgataatt gtttgagggg aggagatgga aacaatgtgg agtctccctc 1560
 tgattggttt tggggaaatg tggagaagag tgccctgctt tgcaaaccatc aacctggcaa 1620
 aaatgcaaca aatgaatttt ccacgcagtt ctttccatgg gcataggtaa gctgtgcctt 1680
 cagctgttgc agatgaaatg ttctgttcac cctgcattac atgtgtttat tcatccagca 1740
 gtgttgctca gctectacct ctgtgccagg gcagcatttt catatccaag atcaattccc 1800
 tctctcagca cagcctgggg aggggggtcat tgttctcctc gtccatcagg gatctcagag 1860
 gctcagagac tgcaagctgc ttgcccaggt cacacagcta gtgaagacca gagcagtttc 1920
 atctggttgt gactctaagc tcagtgtctc ctccactacc ccacaccagc cttggtgcc 1980
 ccaaaagtgc tccccaaaag gaaggagaat gggatttttc ttgaggcatg cacatctgga 2040
 attaaggta aactaattct cacatccctc taaaagtaaa ctactgttag gaacagcagt 2100
 gttctcacag tgtggggcag ccgtccttct aatgaagaca atgatattga cactgtccct 2160
 ctttggcagt tgcattagta actttgaaag gtatatgact gagcgtagca tacaggttaa 2220
 cctgcagaaa cagtacttag gtaattgtag ggcgaggatt ataaatgaaa tttgcaaaat 2280
 cacttagcag caactgaaga caattatcaa ccacgtggag aaaatcaaac cgagcagggc 2340
 tgtgtgaaac atggttgtaa tatgcgactg cgaacactga actctacgcc actccacaaa 2400
 tgatgttttc aggtgtcatg gactgttgcc accatgtatt catccagagt tcttaaagtt 2460
 taaagttgca catgattgta taagcatgct ttctttgagt tttaaattat gtataaacat 2520
 aagttgcatt tagaaatcaa gcataaatca cttcaactgc aaaaaaaaaa aaaaaaaaaa 2580
 aaaaaa 2586

<210> 236

<211> 350

<212> PRT

<213> Homo sapiens

<400> 236

Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala
 1 5 10 15

Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
 20 25 30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
 35 40 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
 50 55 60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
 65 70 75 80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
 85 90 95
 Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His
 100 105 110
 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
 115 120 125
 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
 130 135 140
 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
 145 150 155 160
 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
 165 170 175
 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
 180 185 190
 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
 195 200 205
 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
 210 215 220
 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
 225 230 235 240
 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
 245 250 255
 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
 260 265 270
 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
 275 280 285
 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
 290 295 300
 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
 305 310 315 320
 Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu
 325 330 335
 Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile
 340 345 350

<210> 237

<211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 237
 ggagctgcac cccttgc 17

 <210> 238
 <211> 49
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 238
 ggaggactgt gccaccatga gagactcttc aaaccaagg caaaattgg 49

 <210> 239
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 239
 gcagagcggg gatgcagcgg ctg 24

 <210> 240
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 240
 ttggcagctt catggagg 18

 <210> 241
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 241
 cctgggcaaa aatgcaac 18

<210> 242
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 242
 ctccagctcc tggcgacact cctc

24

<210> 243
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 243
 ggctctcagc taccgcgag gagcgaggcc accctcaatg agatg

45

<210> 244
 <211> 3679
 <212> DNA
 <213> Homo Sapien

<400> 244
 aaggaggctg ggaggaaaga ggtaagaaag gttagagaac ctacctcaca 50
 tctctctggg ctccagaagga ctctgaagat aacaataatt tcagcccatc 100
 cactctcctt ccttcccaaa cacacatgtg catgtacaca cacacataca 150
 cacacataca ctttctcttc cttcactgaa gactcacagt cactcactct 200
 gtgagcaggt catagaaaag gacactaaag ccttaaggac aggcttggcc 250
 attacctctg cagctccttt ggcttggtga gtcaaaaaac atgggagggg 300
 ccaggcacgg tgactcacac ctgtaatccc agcatttttg gagaccgagg 350
 tgagcagatc acttgaggtc aggagttcga gaccagctg gccaacatgg 400
 agaaaccccc atctctacta aaaatacaaa aattagccag gagtgggtggc 450
 aggtgcctgt aatcccagct actcaggtgg ctgagccagg agaatcgctt 500
 gaatccagga ggcggaggat gcagtcagct gagtgcaccg ctgcactcca 550
 gcctgggtga cagaatgaga ctctgtctca aacaaacaaa cacgggagga 600

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

ggggtagata ctgcttctct gcaacctcct taactctgca tctctttctt 650
 ccagggctgc ccctgatggg gcctggcaat gactgagcag gccagcccc 700
 agaggacaag gaagagaagg catattgagg agggcaagaa gtgacgcccc 750
 gtgtagaatg actgccctgg gaggggtggtt ccttgggccc tggcaggggtt 800
 gctgaccctt accctgcaaa acacaaagag caggactcca gactctcctt 850
 gtgaatggtc ccctgccctg cagctccacc atgaggcttc tegtggcccc 900
 actcttgcta gcttgggtgg ctggtgccac tgccactgtg cccgtggtag 950
 cctggcatgt tccctgcccc cctcagtgtg cctgccagat ccggccctgg 1000
 tatacgcgcc gctcgtccta ccgcgaggct accactgtgg actgcaatga 1050
 cctattcctg acggcagtc ccccggcact ccccgcaggc acacagaccc 1100
 tgctcctgca gagcaacagc attgtccgtg tggaccagag tgagctgggc 1150
 tacctggcca atctcacaga gctggacctg tcccagaaca gcttttcgga 1200
 tgcccgagac tgtgatttcc atgccctgcc ccagctgctg agcctgcacc 1250
 tagaggagaa ccagctgacc cggctggagg accacagctt tgcagggctg 1300
 gccagcctac aggaactcta tctcaaccac aaccagctct accgcatcgc 1350
 cccaggggcc ttttctggcc tcagcaactt gctgcggctg cacctcaact 1400
 ccaacctcct gagggccatt gacagccgct ggtttgaaat gctgccaac 1450
 ttggagatac tcatgattgg cggcaacaag gtagatgcca tcctggacat 1500
 gaacttccgg cccttgcca acctgcgtag cctggtgcta gcaggcatga 1550
 acctgcggga gatctccgac tatgccctgg aggggctgca aagcctggag 1600
 agcctctcct tctatgacaa ccagctggcc cgggtgcca ggcgggcact 1650
 ggaacagggtg cccgggctca agttcctaga cctcaacaag aaccgctcc 1700
 agcgggtagg gccgggggac tttgccaaca tgctgcacct taaggagctg 1750
 ggactgaaca acatggagga gctggtctcc atcgacaagt ttgccctgg 1800
 gaacctcccc gagctgacca agctggacat caccaataac ccacggctgt 1850
 ccttcatcca ccccgcgcc ttccaccacc tgccccagat ggagaccctc 1900
 atgctcaaca acaacgctct cagtgccttg caccagcaga cgggtggagt 1950

cctgccaac ctgcaggagg taggtctcca cggcaacccc atccgctgtg 2000
 actgtgtcat ccgctggggc aatgccacgg gcacccgtgt ccgcttcatc 2050
 gagccgcaat ccaccctgtg tgcggagcct ccggacctcc agcgctccc 2100
 ggtccgtgag gtgcccttcc gggagatgac ggaccactgt ttgcccctca 2150
 tctccccacg aagcttcccc ccaagcctcc aggtagccag tggagagagc 2200
 atggtgctgc attgccgggc actggccgaa cccgaacccg agatctactg 2250
 ggtaactcca gctgggcttc gactgacacc tgcccatgca ggcaggaggt 2300
 accgggtgta ccccgagggg accctggagc tgcggagggt gacagcagaa 2350
 gaggcagggc tatacacctg tgtggcccag aacctggtgg gggctgacac 2400
 taagacggtt agtgtggttg tgggccgtgc tctcctccag ccaggcaggg 2450
 acgaaggaca ggggctggag ctccgggtgc aggagaccca cccctatcac 2500
 atcctgctat cttgggtcac cccaccaac acagtgtcca ccaacctcac 2550
 ctggtccagt gcctcctccc tccggggcca gggggccaca gctctggccc 2600
 gcctgcctcg gggaaaccac agctacaaca ttaccgcct ccttcaggcc 2650
 acggagtact gggcctgcct gcaagtggcc tttgctgatg cccacacca 2700
 gttggcttgt gtatgggcca ggaccaaaga ggccacttct tgccacagag 2750
 ccttagggga tcgtcctggg ctcatgcca tcctggctct cgctgtcctt 2800
 ctctggcag ctgggctagc ggcccacctt ggcacaggcc aaccagga 2850
 ggggtgtgggt gggaggcggc ctctccctcc agcctgggct ttctggggct 2900
 ggagtgcccc ttctgtccgg gttgtgtctg ctcccctcgt cctgccctgg 2950
 aatccaggga ggaagctgcc cagatcctca gaaggggaga cactgttgcc 3000
 accattgtct caaaattctt gaagctcagc ctgttctcag cagtagagaa 3050
 atcactagga ctacttttta ccaaaagaga agcagtctgg gccagatgcc 3100
 ctgccaggaa agggacatgg acccacgtgc ttgaggcctg gcagctgggc 3150
 caagacagat ggggctttgt ggccctgggg gtgcttctgc agccttgaaa 3200
 aagttgccct tacctcctag ggtaacctct gctgccattc tgagggaacat 3250

<210> 245

<212> PRT

<213> Homo Sapien

<400> 245

Ala Thr Ala Thr Val Pro Val Val Pro Trp His Val Pro Cys Pro
20 25 30

Pro Gln Cys Ala Cys Gln Ile Arg Pro Trp Tyr Thr Pro Arg Ser
35 40 45

Ser Tyr Arg Glu Ala Thr Thr Val Asp Cys Asn Asp Leu Phe Leu
50 55 60

Thr Ala Val Pro Pro Ala Leu Pro Ala Gly Thr Gln Thr Leu Leu
65 70 75

Leu Gln Ser Asn Ser Ile Val Arg Val Asp Gln Ser Glu Leu Gly
80 85 90

Tyr Leu Ala Asn Leu Thr Glu Leu Asp Leu Ser Gln Asn Ser Phe
95 100 105

Ser Asp Ala Arg Asp Cys Asp Phe His Ala Leu Pro Gln Leu Leu
110 115 120

Ser Leu His Leu Glu Glu Asn Gln Leu Thr Arg Leu Glu Asp His
125 130 135

Ser Phe Ala Gly Leu Ala Ser Leu Gln Glu Leu Tyr Leu Asn His
140 145 150

Asn	Gln	Leu	Tyr	Arg	Ile	Ala	Pro	Arg	Ala	Phe	Ser	Gly	Leu	Ser	
				155					160					165	
Asn	Leu	Leu	Arg	Leu	His	Leu	Asn	Ser	Asn	Leu	Leu	Arg	Ala	Ile	
				170					175					180	
Asp	Ser	Arg	Trp	Phe	Glu	Met	Leu	Pro	Asn	Leu	Glu	Ile	Leu	Met	
				185					190					195	
Ile	Gly	Gly	Asn	Lys	Val	Asp	Ala	Ile	Leu	Asp	Met	Asn	Phe	Arg	
				200					205					210	
Pro	Leu	Ala	Asn	Leu	Arg	Ser	Leu	Val	Leu	Ala	Gly	Met	Asn	Leu	
				215					220					225	
Arg	Glu	Ile	Ser	Asp	Tyr	Ala	Leu	Glu	Gly	Leu	Gln	Ser	Leu	Glu	
				230					235					240	
Ser	Leu	Ser	Phe	Tyr	Asp	Asn	Gln	Leu	Ala	Arg	Val	Pro	Arg	Arg	
				245					250					255	
Ala	Leu	Glu	Gln	Val	Pro	Gly	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys	
				260					265					270	
Asn	Pro	Leu	Gln	Arg	Val	Gly	Pro	Gly	Asp	Phe	Ala	Asn	Met	Leu	
				275					280					285	
His	Leu	Lys	Glu	Leu	Gly	Leu	Asn	Asn	Met	Glu	Glu	Leu	Val	Ser	
				290					295					300	
Ile	Asp	Lys	Phe	Ala	Leu	Val	Asn	Leu	Pro	Glu	Leu	Thr	Lys	Leu	
				305					310					315	
Asp	Ile	Thr	Asn	Asn	Pro	Arg	Leu	Ser	Phe	Ile	His	Pro	Arg	Ala	
				320					325					330	
Phe	His	His	Leu	Pro	Gln	Met	Glu	Thr	Leu	Met	Leu	Asn	Asn	Asn	
				335					340					345	
Ala	Leu	Ser	Ala	Leu	His	Gln	Gln	Thr	Val	Glu	Ser	Leu	Pro	Asn	
				350					355					360	
Leu	Gln	Glu	Val	Gly	Leu	His	Gly	Asn	Pro	Ile	Arg	Cys	Asp	Cys	
				365					370					375	
Val	Ile	Arg	Trp	Ala	Asn	Ala	Thr	Gly	Thr	Arg	Val	Arg	Phe	Ile	
				380					385					390	
Glu	Pro	Gln	Ser	Thr	Leu	Cys	Ala	Glu	Pro	Pro	Asp	Leu	Gln	Arg	
				395					400					405	
Leu	Pro	Val	Arg	Glu	Val	Pro	Phe	Arg	Glu	Met	Thr	Asp	His	Cys	

410										415				420			
Leu	Pro	Leu	Ile	Ser	Pro	Arg	Ser	Phe	Pro	Pro	Ser	Leu	Gln	Val			
				425					430					435			
Ala	Ser	Gly	Glu	Ser	Met	Val	Leu	His	Cys	Arg	Ala	Leu	Ala	Glu			
				440					445					450			
Pro	Glu	Pro	Glu	Ile	Tyr	Trp	Val	Thr	Pro	Ala	Gly	Leu	Arg	Leu			
				455					460					465			
Thr	Pro	Ala	His	Ala	Gly	Arg	Arg	Tyr	Arg	Val	Tyr	Pro	Glu	Gly			
				470					475					480			
Thr	Leu	Glu	Leu	Arg	Arg	Val	Thr	Ala	Glu	Glu	Ala	Gly	Leu	Tyr			
				485					490					495			
Thr	Cys	Val	Ala	Gln	Asn	Leu	Val	Gly	Ala	Asp	Thr	Lys	Thr	Val			
				500					505					510			
Ser	Val	Val	Val	Gly	Arg	Ala	Leu	Leu	Gln	Pro	Gly	Arg	Asp	Glu			
				515					520					525			
Gly	Gln	Gly	Leu	Glu	Leu	Arg	Val	Gln	Glu	Thr	His	Pro	Tyr	His			
				530					535					540			
Ile	Leu	Leu	Ser	Trp	Val	Thr	Pro	Pro	Asn	Thr	Val	Ser	Thr	Asn			
				545					550					555			
Leu	Thr	Trp	Ser	Ser	Ala	Ser	Ser	Leu	Arg	Gly	Gln	Gly	Ala	Thr			
				560					565					570			
Ala	Leu	Ala	Arg	Leu	Pro	Arg	Gly	Thr	His	Ser	Tyr	Asn	Ile	Thr			
				575					580					585			
Arg	Leu	Leu	Gln	Ala	Thr	Glu	Tyr	Trp	Ala	Cys	Leu	Gln	Val	Ala			
				590					595					600			
Phe	Ala	Asp	Ala	His	Thr	Gln	Leu	Ala	Cys	Val	Trp	Ala	Arg	Thr			
				605					610					615			
Lys	Glu	Ala	Thr	Ser	Cys	His	Arg	Ala	Leu	Gly	Asp	Arg	Pro	Gly			
				620					625					630			
Leu	Ile	Ala	Ile	Leu	Ala	Leu	Ala	Val	Leu	Leu	Leu	Ala	Ala	Gly			
				635					640					645			
Leu	Ala	Ala	His	Leu	Gly	Thr	Gly	Gln	Pro	Arg	Lys	Gly	Val	Gly			
				650					655					660			
Gly	Arg	Arg	Pro	Leu	Pro	Pro	Ala	Trp	Ala	Phe	Trp	Gly	Trp	Ser			
				665					670					675			

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

gtgatcaagt tcatcctcat catctgctac accgtctact acgtgcacaa 150

catcaagttc gacgtggact gcaccgtgga cattgagagc ctgacgggct 200
 accgcaccta ccgctgtgcc caccocctgg ccacactctt caagatcctg 250
 gcgtccttct acatcagcct agtcatcttc tacggcctca tctgcatgta 300
 cacactgtgg tggatgctac ggcgctccct caagaagtac tcgtttgagt 350
 cgatccgtga ggagagcagc tacagcgaca tccccgacgt caagaacgac 400
 ttcgccttca tgctgcacct cattgaccaa tacgacccgc tctactccaa 450
 gcgcttcgcc gtcttctgtt cggaggtgag tgagaacaag ctgcggcagc 500
 tgaacctcaa caacgagtgg acgttggaac agctccggca gcggctcacc 550
 aagaacgcgc aggacaagct ggagctgcac ctgttcatgc tcagtggcat 600
 ccctgacact gtgtttgacc tgggtggagct ggaggtcctc aagctggagc 650
 tgatccccga cgtgaccatc ccgcccagca ttgcccagct cacgggcctc 700
 aaggagctgt ggctctacca cacagcggcc aagattgaag cgctgcgct 750
 ggcttctctg cgcgagaacc tgcgggcgct gcacatcaag ttcaccgaca 800
 tcaaggagat cccgctgtgg atctatagcc tgaagacact ggaggagctg 850
 cacctgacgg gcaacctgag cgcggagaac aaccgctaca tcgtcatcga 900
 cgggctgcgg gagctcaaac gcctcaaggt gctgcggctc aagagcaacc 950
 taagcaagct gccacaggtg gtcacagatg tgggcgtgca cctgcagaag 1000
 ctgtccatca acaatgaggg caccaagctc atcgtcctca acagcctcaa 1050
 gaagatggcg aacctgactg agctggagct gatccgctgc gacctggagc 1100
 gcatcccca ctccatcttc agcctccaca acctgcagga gattgacctc 1150
 aaggacaaca acctcaagac catcgaggag atcatcagct tccagcacct 1200
 gcaccgcctc acctgcctta agctgtggta caaccacatc gcctacatcc 1250
 ccatccagat cggcaacctc accaacctgg agcgctctta cctgaaccgc 1300
 aacaagatcg agaagatccc caccagctc ttctactgcc gcaagctgcg 1350
 ctacctggac ctacgccaca acaacctgac ctctctccct gccgacatcg 1400
 gcctcctgca gaacctccag aacctagcca tcacggccaa ccggatcgag 1450

acgctccctc cggagctctt ccagtgccgg aagctgcggg cctgcacct 1500
 gggcaacaac gtgctgcagt cactgccctc caggggtgggc gagctgacca 1550
 acctgacgca gatcgagctg cggggcaacc ggctggagtg cctgcctgtg 1600
 gagctgggag agtgcccact gctcaagcgc agcggccttg tggaggagga 1650
 ggacctgttc aacacactgc caccgaggt gaaggagcgg ctgtggaggg 1700
 ctgacaagga gcaggcctga gcgaggccgg cccagcacag caagcagcag 1750
 gaccgctgcc cagtcctcag gcccgagggg gcaggcctag cttctccag 1800
 aactcccgga cagccaggac agcctcgcgg ctgggcagga gcctggggcc 1850
 gcttgtgagt caggccagag cgagaggaca gtatctgtgg ggctggcccc 1900
 tttctccct ctgagactca cgtccccag ggcaagtgt tgtggaggag 1950
 agcaagtctc aagagcgcag tatttgata atcagggtct cctccctgga 2000
 ggccagctct gcccagggg ctgagctgcc accagaggtc ctgggacct 2050
 cactttagtt cttggtattt atttttctcc atctcccacc tcttcatcc 2100
 agataactta tacattccca agaaagtcca gccagatgg aaggtgttca 2150
 gggaaagggt ggctgccttt tcccctgtc cttatttagc gatgccgccg 2200
 ggcatttaac acccacctgg acttcagcag agtggtccgg ggccaaccag 2250
 ccatgggacg gtcaccacgc agtgccgggc tgggctctgc ggtgcggtcc 2300
 acgggagagc aggccctccag ctggaaaggc caggcctgga gcttgcctct 2350
 tcagtttttg tggcagtttt agttttttgt tttttttttt tttaatcaaa 2400
 aaacaatttt ttttaaaaaa aagctttgaa aatggatggg ttgggtatta 2450
 aaaagaaaaa aaaaacttaa aaaaaaaaag acactaacgg ccagtgagtt 2500
 ggagtctcag ggcagggtgg cagtttccct tgagcaaagc agccagacgt 2550
 tgaactgtgt ttcccttccc tgggcgcagg gtgcagggtg tcttccggat 2600
 ctggtgtgac cttggtccag gagttctatt tgttccctgg gagggaggtt 2650
 tttttgtttg ttttttgggt ttttttgggt tcttgttttc tttctcctcc 2700
 atgtgtcttg gcaggcactc atttctgtgg ctgtcggcca gagggaatgt 2750
 tctggagctg ccaaggaggg aggagactcg gggtggctaa tccccggatg 2800

	95		100		105
Asn Asp Phe Ala	Phe Met Leu His Leu	Ile Asp Gln Tyr Asp	Pro		
	110		115		120
Leu Tyr Ser Lys	Arg Phe Ala Val Phe	Leu Ser Glu Val Ser	Glu		
	125		130		135
Asn Lys Leu Arg	Gln Leu Asn Leu Asn	Asn Glu Trp Thr Leu	Asp		
	140		145		150
Lys Leu Arg Gln	Arg Leu Thr Lys Asn	Ala Gln Asp Lys Leu	Glu		
	155		160		165
Leu His Leu Phe	Met Leu Ser Gly Ile	Pro Asp Thr Val Phe	Asp		
	170		175		180
Leu Val Glu Leu	Glu Val Leu Lys Leu	Glu Leu Ile Pro Asp	Val		
	185		190		195
Thr Ile Pro Pro	Ser Ile Ala Gln Leu	Thr Gly Leu Lys Glu	Leu		
	200		205		210
Trp Leu Tyr His	Thr Ala Ala Lys Ile	Glu Ala Pro Ala Leu	Ala		
	215		220		225
Phe Leu Arg Glu	Asn Leu Arg Ala Leu	His Ile Lys Phe Thr	Asp		
	230		235		240
Ile Lys Glu Ile	Pro Leu Trp Ile Tyr	Ser Leu Lys Thr Leu	Glu		
	245		250		255
Glu Leu His Leu	Thr Gly Asn Leu Ser	Ala Glu Asn Asn Arg	Tyr		
	260		265		270
Ile Val Ile Asp	Gly Leu Arg Glu Leu	Lys Arg Leu Lys Val	Leu		
	275		280		285
Arg Leu Lys Ser	Asn Leu Ser Lys Leu	Pro Gln Val Val Thr	Asp		
	290		295		300
Val Gly Val His	Leu Gln Lys Leu Ser	Ile Asn Asn Glu Gly	Thr		
	305		310		315
Lys Leu Ile Val	Leu Asn Ser Leu Lys	Lys Met Ala Asn Leu	Thr		
	320		325		330
Glu Leu Glu Leu	Ile Arg Cys Asp Leu	Glu Arg Ile Pro His	Ser		
	335		340		345
Ile Phe Ser Leu	His Asn Leu Gln Glu	Ile Asp Leu Lys Asp	Asn		
	350		355		360

Asn	Leu	Lys	Thr	Ile	Glu	Glu	Ile	Ile	Ser	Phe	Gln	His	Leu	His
				365					370					375
Arg	Leu	Thr	Cys	Leu	Lys	Leu	Trp	Tyr	Asn	His	Ile	Ala	Tyr	Ile
				380					385					390
Pro	Ile	Gln	Ile	Gly	Asn	Leu	Thr	Asn	Leu	Glu	Arg	Leu	Tyr	Leu
				395					400					405
Asn	Arg	Asn	Lys	Ile	Glu	Lys	Ile	Pro	Thr	Gln	Leu	Phe	Tyr	Cys
				410					415					420
Arg	Lys	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	His	Asn	Asn	Leu	Thr	Phe
				425					430					435
Leu	Pro	Ala	Asp	Ile	Gly	Leu	Leu	Gln	Asn	Leu	Gln	Asn	Leu	Ala
				440					445					450
Ile	Thr	Ala	Asn	Arg	Ile	Glu	Thr	Leu	Pro	Pro	Glu	Leu	Phe	Gln
				455					460					465
Cys	Arg	Lys	Leu	Arg	Ala	Leu	His	Leu	Gly	Asn	Asn	Val	Leu	Gln
				470					475					480
Ser	Leu	Pro	Ser	Arg	Val	Gly	Glu	Leu	Thr	Asn	Leu	Thr	Gln	Ile
				485					490					495
Glu	Leu	Arg	Gly	Asn	Arg	Leu	Glu	Cys	Leu	Pro	Val	Glu	Leu	Gly
				500					505					510
Glu	Cys	Pro	Leu	Leu	Lys	Arg	Ser	Gly	Leu	Val	Val	Glu	Glu	Asp
				515					520					525
Leu	Phe	Asn	Thr	Leu	Pro	Pro	Glu	Val	Lys	Glu	Arg	Leu	Trp	Arg
				530					535					540
Ala	Asp	Lys	Glu	Gln	Ala									
				545										

<210> 251

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 251

caacaatgag ggcaccaagc 20

<210> 252

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 252

gatggctagg ttctggaggt tctg 24

<210> 253

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 253

caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<210> 254

<211> 1650

<212> DNA

<213> Homo Sapien

<400> 254

gcctgttgct gatgctgccg tgcggtactt gtcattggagc tggcactgcg 50
 gcgctctccc gtcccgcggg ggttgcctgct gctgccgctg ctgctggggc 100
 tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150
 tgggattatg tgacgggtccg caaggatgcc tacatgttct ggtggctcta 200
 ttatgccacc aactcctgca agaacttctc agaactgccc ctggtcatgt 250
 ggcttcaggg cgggtccaggc ggttctagca ctggatttgg aaactttgag 300
 gaaattgggc cccttgacag tgatctcaaa ccacggaaaa ccacctggct 350
 ccaggctgcc agtctcctat ttgtggataa tcccgtgggc actgggttca 400
 gttatgtgaa tggtagtggt gcctatgcca aggacctggc tatggtggct 450
 tcagacatga tggttctcct gaagaccttc ttcagttgcc acaaagaatt 500
 ccagacagtt ccattctaca ttttctcaga gtccatgga ggaaaaatgg 550
 cagctggcat tggctagag ctttataagg ccattcagcg agggaccatc 600
 aagtgcaact ttgcgggggt tgccttgggt gattcctgga tctccctgt 650
 tgattcgggt ctctcctggg gaccttacct gtacagcatg tctcttctcg 700

153

aagacaaagg tctggcagag gtgtctaagg ttgcagagca agtactgaat 750
gccgtaaata aggggctcta cagagaggcc acagagctgt gggggaaaagc 800
agaaatgatac attgaacaga acacagatgg ggtgaacttc tataacatct 850
taactaaaag cactcccacg tctacaatgg agtcgagtct agaattcaca 900
cagagccacc tagtttgtct ttgtcagcgc cacgtgagac acctacaacg 950
agatgcctta agccagctca tgaatggccc catcagaaaag aagctcaaaa 1000
ttattcctga ggatcaatcc tggggaggcc aggctaccaa cgtctttgtg 1050
aacatggagg aggacttcat gaagccagtc attagcattg tggacgagtt 1100
gctggaggca gggatcaacg tgacggtgta taatggacag ctggatctca 1150
tcgtagatac catgggtcag gaggcctggg tgcggaaact gaagtggcca 1200
gaactgccta aattcagtca gctgaagtgg aaggccctgt acagtgaccc 1250
taaactcttg gaaacatctg cttttgtcaa gtcctacaag aaccttgctt 1300
tctactggat tctgaaagct ggtcatatgg ttccttctga ccaaggggac 1350
atggctctga agatgatgag actggtgact cagcaagaat aggatggatg 1400
gggctggaga tgagctggtt tggccttggg gcacagagct gagctgaggc 1450
cgctgaagct gtaggaagcg ccattcttcc ctgtatctaa ctggggctgt 1500
gatcaagaag gttctgacca gcttctgcag aggataaaat cattgtctct 1550
ggaggcaatt tggaaattat ttctgcttct taaaaaaacc taagattttt 1600
taaaaaattg atttgttttg atcaaaataa aggatgataa tagatattaa 1650

<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

Met	Glu	Leu	Ala	Leu	Arg	Arg	Ser	Pro	Val	Pro	Arg	Trp	Leu	Leu
1				5					10				15	
Leu	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp
			20						25				30	
Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
			35						40				45	

Arg	Lys	Asp	Ala	Tyr 50	Met	Phe	Trp	Trp	Leu 55	Tyr	Tyr	Ala	Thr	Asn 60
Ser	Cys	Lys	Asn	Phe 65	Ser	Glu	Leu	Pro	Leu 70	Val	Met	Trp	Leu	Gln 75
Gly	Gly	Pro	Gly	Gly 80	Ser	Ser	Thr	Gly	Phe 85	Gly	Asn	Phe	Glu	Glu 90
Ile	Gly	Pro	Leu	Asp 95	Ser	Asp	Leu	Lys	Pro 100	Arg	Lys	Thr	Thr	Trp 105
Leu	Gln	Ala	Ala	Ser 110	Leu	Leu	Phe	Val	Asp 115	Asn	Pro	Val	Gly	Thr 120
Gly	Phe	Ser	Tyr	Val 125	Asn	Gly	Ser	Gly	Ala 130	Tyr	Ala	Lys	Asp	Leu 135
Ala	Met	Val	Ala	Ser 140	Asp	Met	Met	Val	Leu 145	Leu	Lys	Thr	Phe	Phe 150
Ser	Cys	His	Lys	Glu 155	Phe	Gln	Thr	Val	Pro 160	Phe	Tyr	Ile	Phe	Ser 165
Glu	Ser	Tyr	Gly	Gly 170	Lys	Met	Ala	Ala	Gly 175	Ile	Gly	Leu	Glu	Leu 180
Tyr	Lys	Ala	Ile	Gln 185	Arg	Gly	Thr	Ile	Lys 190	Cys	Asn	Phe	Ala	Gly 195
Val	Ala	Leu	Gly	Asp 200	Ser	Trp	Ile	Ser	Pro 205	Val	Asp	Ser	Val	Leu 210
Ser	Trp	Gly	Pro	Tyr 215	Leu	Tyr	Ser	Met	Ser 220	Leu	Leu	Glu	Asp	Lys 225
Gly	Leu	Ala	Glu	Val 230	Ser	Lys	Val	Ala	Glu 235	Gln	Val	Leu	Asn	Ala 240
Val	Asn	Lys	Gly	Leu 245	Tyr	Arg	Glu	Ala	Thr 250	Glu	Leu	Trp	Gly	Lys 255
Ala	Glu	Met	Ile	Ile 260	Glu	Gln	Asn	Thr	Asp 265	Gly	Val	Asn	Phe	Tyr 270
Asn	Ile	Leu	Thr	Lys 275	Ser	Thr	Pro	Thr	Ser 280	Thr	Met	Glu	Ser	Ser 285
Leu	Glu	Phe	Thr	Gln 290	Ser	His	Leu	Val	Cys 295	Leu	Cys	Gln	Arg	His 300
Val	Arg	His	Leu	Gln	Arg	Asp	Ala	Leu	Ser	Gln	Leu	Met	Asn	Gly

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile	Pro Glu Asp Gln Ser Trp	
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val	Asn Met Glu Glu Asp Phe	
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp	Glu Leu Leu Glu Ala Gly	
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln	Leu Asp Leu Ile Val Asp	
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg	Lys Leu Lys Trp Pro Glu	
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp	Lys Ala Leu Tyr Ser Asp	
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe	Val Lys Ser Tyr Lys Asn	
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala	Gly His Met Val Pro Ser	
425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met	Met Arg Leu Val Thr Gln	
440	445	450

Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

```

ggccgcggga gaggaggcca tgggcgcgcg cggggcgctg ctgctggcgc 50
tgctgctggc tcgggctgga ctcaggaagc cggagtcgca ggaggcggcg 100
ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150
tggagaggac gccgaactcg ggcgttggcc gtggcagggg agcctgcgcc 200
tgtgggattc ccacgtatgc ggagtgaacc tgctcagcca ccgctgggca 250
ctcaeggcgg cgcactgctt tgaaacctat agtgacctta gtgatccctc 300
cgggtggatg gtccagtttg gccagctgac ttccatgcca tccttctgga 350
gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400

```


cctcgtacc tggggaattc accctatgac attgccttgg tgaagctgtc 450
 tgcacctgtc acctacacta aacacatcca gcccatctgt ctccaggcct 500
 ccacatttga gtttgagaac cggacagact gctgggtgac tggctggggg 550
 tacatcaaag aggatgagge actgccatct cccacacccc tccaggaagt 600
 tcaggtegcc atcataaaca actctatgtg caaccacctc ttcctcaagt 650
 acagtttccg caaggacatc tttggagaca tggtttgtgc tggcaacgcc 700
 caaggcggga aggatgcctg ctloggtgac tcagggtggac ccttggcctg 750
 taacaagaat ggactgtggg atcagattgg agtcgtgagc tggggagtgg 800
 gctgtggteg gcccaatcgg ccggtgtct acaccaatat cagccaccac 850
 tttgagtga tccagaagct gatggcccag agtggcatgt cccagccaga 900
 cccctcctgg ccaactactct tttccctct tctctgggct ctcccactcc 950
 tggggccggg ctgagcctac ctgagcccat gcagcctggg gccactgcc 1000
 agtcaggccc tggttctctt ctgtcttgtt tggtaataaa cacattccag 1050
 ttgatgcctt gcagggcatt cttcaaaaaa aaaaaaaaaa aaaaaaaaaa 1100

<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg
 1 5 10 15

Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser
 20 25 30

Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly
 35 40 45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg
 50 55 60

Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg
 65 70 75

Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu
 80 85 90

F00120-220000

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser
 95 100 105
 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe
 110 115 120
 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro
 125 130 135
 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr
 140 145 150
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe
 155 160 165
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys
 170 175 180
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln
 185 190 195
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys
 200 205 210
 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly
 215 220 225
 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
 230 235 240
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val
 245 250 255
 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val
 260 265 270
 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met
 275 280 285
 Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu
 290 295 300
 Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
 305 310

<210> 258

<211> 2427

<212> DNA

<213> Homo Sapien

<400> 258

cccacgcgtc cgcggacgcg tgggaagggc agaatgggac tccaagcctg 50

tgatggctac tgggtggtca gcaacagagt gccattcca tgggtgtccg 1450
 gaacctcggc ctctactcca gtgtttgggg ggatcctatc cttgatcaat 1500
 gagcacagga tccttagtgg ccgccccctt cttggctttc tcaacccaag 1550
 gctctaccag cagcatgggg caggtctctt tgatgtaacc cgtggctgcc 1600
 atgagtccctg tctggatgaa gaggtagagg gccagggttt ctgctctggt 1650
 cctggctggg atcctgtaac aggctgggga acaccaactt occagctttg 1700
 ctgaagactc tactcaacce ctgacccttt cctatcagga gagatggctt 1750
 gtccctgcc ctgaagctgg cagttcagtc ccttattctg cctgtttgga 1800
 agcctgctg aacctcaac tattgactgc tgcagacagc ttatctccct 1850
 aacctgaaa tgctgtgagc ttgacttgac tcccaacctt accatgctcc 1900
 atcatactca ggtctcccta ctctgctt agattctca ataagatgct 1950
 gtaactagca ttttttgaat gcctctccct ccgcatctca tctttctctt 2000
 ttcaatcagg cttttccaaa gggttgtata cagactctgt gcactatttc 2050
 acttgatatt cattcccca ttcactgcaa ggagacctct actgtcacgc 2100
 tttactcttt cctacctga catccagaaa caatggctc cagtgcatac 2150
 ttctcaatct ttgctttatg gcctttccat catagttgcc cactccctct 2200
 ccttacttag ctccaggtc ttaacttctc tgactactct tgtcttctc 2250
 tctcatcaat ttctgcttct tcatggaatg ctgaccttca ttgctccatt 2300
 tgtagatttt tgctcttctc agtttactca ttgtccctg gaacaaatca 2350
 ctgacatcta caaccattac catctcacta aataagactt tctatccaat 2400
 aatgattgat acctcaaag taaaaaa 2427

<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

Met	Gly	Leu	Gln	Ala	Cys	Leu	Leu	Gly	Leu	Phe	Ala	Leu	Ile	Leu
1					5				10				15	

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

	20		25		30
Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu	35		40		45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg	50		55		60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln	65		70		75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg	80		85		90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala	95		100		105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu	110		115		120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly	125		130		135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val	140		145		150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro	155		160		165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser	170		175		180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly	185		190		195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn	200		205		210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln	215		220		225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu	230		235		240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala	245		250		255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly	260		265		270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala	275		280		285

Asn	Ile	Ser	Thr	Trp	Val	Tyr	Ser	Ser	Pro	Gly	Arg	His	Glu	Gly	
				290					295					300	
Gln	Glu	Pro	Phe	Leu	Gln	Trp	Leu	Met	Leu	Leu	Ser	Asn	Glu	Ser	
				305					310					315	
Ala	Leu	Pro	His	Val	His	Thr	Val	Ser	Tyr	Gly	Asp	Asp	Glu	Asp	
				320					325					330	
Ser	Leu	Ser	Ser	Ala	Tyr	Ile	Gln	Arg	Val	Asn	Thr	Glu	Leu	Met	
				335					340					345	
Lys	Ala	Ala	Ala	Arg	Gly	Leu	Thr	Leu	Leu	Phe	Ala	Ser	Gly	Asp	
				350					355					360	
Ser	Gly	Ala	Gly	Cys	Trp	Ser	Val	Ser	Gly	Arg	His	Gln	Phe	Arg	
				365					370					375	
Pro	Thr	Phe	Pro	Ala	Ser	Ser	Pro	Tyr	Val	Thr	Thr	Val	Gly	Gly	
				380					385					390	
Thr	Ser	Phe	Gln	Glu	Pro	Phe	Leu	Ile	Thr	Asn	Glu	Ile	Val	Asp	
				395					400					405	
Tyr	Ile	Ser	Gly	Gly	Gly	Phe	Ser	Asn	Val	Phe	Pro	Arg	Pro	Ser	
				410					415					420	
Tyr	Gln	Glu	Glu	Ala	Val	Thr	Lys	Phe	Leu	Ser	Ser	Ser	Pro	His	
				425					430					435	
Leu	Pro	Pro	Ser	Ser	Tyr	Phe	Asn	Ala	Ser	Gly	Arg	Ala	Tyr	Pro	
				440					445					450	
Asp	Val	Ala	Ala	Leu	Ser	Asp	Gly	Tyr	Trp	Val	Val	Ser	Asn	Arg	
				455					460					465	
Val	Pro	Ile	Pro	Trp	Val	Ser	Gly	Thr	Ser	Ala	Ser	Thr	Pro	Val	
				470					475					480	
Phe	Gly	Gly	Ile	Leu	Ser	Leu	Ile	Asn	Glu	His	Arg	Ile	Leu	Ser	
				485					490					495	
Gly	Arg	Pro	Pro	Leu	Gly	Phe	Leu	Asn	Pro	Arg	Leu	Tyr	Gln	Gln	
				500					505					510	
His	Gly	Ala	Gly	Leu	Phe	Asp	Val	Thr	Arg	Gly	Cys	His	Glu	Ser	
				515					520					525	
Cys	Leu	Asp	Glu	Glu	Val	Glu	Gly	Gln	Gly	Phe	Cys	Ser	Gly	Pro	
				530					535					540	
Gly	Trp	Asp	Pro	Val	Thr	Gly	Trp	Gly	Thr	Pro	Thr	Ser	Gln	Leu	
				545					550					555	

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

Ser Gly Lys Ser	Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser	125	130	135
Arg Phe Ser Ile	Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe	140	145	150
Ser Thr Ser Val	Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val	155	160	165
Ala Glu Lys His	Val Leu Thr Ala Ala His Cys Ile His Asp Gly	170	175	180
Lys Thr Tyr Val	Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu	185	190	195
Lys Pro Lys Phe	Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr	200	205	210
Ser Ala Met Pro	Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys	215	220	225
Arg Thr His Val	Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp	230	235	240
Ile Gly Met Asp	Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro	245	250	255
His Lys Arg Lys	Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys	260	265	270
Gln Leu Pro Gly	Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp	275	280	285
Arg Pro Gly Asn	Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu	290	295	300
Thr Tyr Asp Leu	Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala	305	310	315
Ser Gly Ser Gly	Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln	320	325	330
Lys Trp Glu Arg	Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp	335	340	345
Val Asp Met Asn	Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg	350	355	360
Ile Thr Pro Leu	Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly	365	370	375
Asn Tyr Leu Asp	Cys Arg Glu Gly	380		

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

Gly	Ser	Ile	Gln	Asp	Gly	Val	Pro	Leu	Pro	His	Pro	Gln	Thr	Leu
				185					190					195
Gln	Lys	Leu	Lys	Val	Pro	Ile	Ile	Asp	Ser	Glu	Val	Cys	Ser	His
				200					205					210
Leu	Tyr	Trp	Arg	Gly	Ala	Gly	Gln	Gly	Pro	Ile	Thr	Glu	Asp	Met
				215					220					225
Leu	Cys	Ala	Gly	Tyr	Leu	Glu	Gly	Glu	Arg	Asp	Ala	Cys	Leu	Gly
				230					235					240
Asp	Ser	Gly	Gly	Pro	Leu	Met	Cys	Gln	Val	Asp	Gly	Ala	Trp	Leu
				245					250					255
Leu	Ala	Gly	Ile	Ile	Ser	Trp	Gly	Glu	Gly	Cys	Ala	Glu	Arg	Asn
				260					265					270
Arg	Pro	Gly	Val	Tyr	Ile	Ser	Leu	Ser	Ala	His	Arg	Ser	Trp	Val
				275					280					285
Glu	Lys	Ile	Val	Gln	Gly	Val	Gln	Leu	Arg	Gly	Arg	Ala	Gln	Gly
				290					295					300
Gly	Gly	Ala	Leu	Arg	Ala	Pro	Ser	Gln	Gly	Ser	Gly	Ala	Ala	Ala
				305					310					315

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

gtccgcaagg atgcctacat gttc 24

<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagaggtgt ctaagggtg 19

<210> 266

<211> 24

168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 266
agctctagac caatgccagc ttcc 24

<210> 267
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 267
gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<210> 268
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 268
ggggaattca ccctatgaca ttgcc 25

<210> 269
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 269
gaatgccctg caagcatcaa ctgg 24

<210> 270
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 270
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 271
gcggaagggc agaatgggac tccaag 26

<210> 272
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 272
cagccctgcc acatgtgc 18

<210> 273
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 273
tactgggtgg tcagcaac 18

<210> 274
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 274
ggcgaagagc agggtgagac cccg 24

<210> 275
<211> 45

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

F02F2205670000

<223> Synthetic Oligonucleotide Probe

<400> 280

ttacagtgcc ccctggaaac ccacttggcc tgcataccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281

cgtctcgagc gctccataca gttcccttgc ccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

tggaggggga gcgggatgct tgtctgggag actccggggg cccctcatg 50

tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

ccctcagacc ctgcagaagc tgaagggtcc tatcatcgac tcggaagtct 50

gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100

atgctgtgtg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50

ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100

agatgaggag aaacgtttga tgggtggagct gcacaacctc taccgggccc 150
 aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200
 ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250
 caaggagcgc gggcgccgcg gcgagaatct gttcgccatc acagacgagg 300
 gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350
 tacaacctca gcgccgccac ctgcagccca ggccagatgt gcggccacta 400
 cacgcaggtg gtatgggcca agacagagag gatcggctgt ggttcccact 450
 tctgtgagaa gctccagggg gttgaggaga ccaacatcga attactggtg 500
 tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550
 ggggactccg tgctcccaat gtccctctgg ctaccactgc aagaactccc 600
 tctgtgaacc catcggaagc ccggaagatg ctcaggattt gccttacctg 650
 gtaactgagg ccccatcctt ccgggcgact gaagcatcag actctaggaa 700
 aatgggtact ccttcttccc tagcaacggg gattccggct ttcttggtaa 750
 cagaggtctc aggtccctg gcaaccaagg ctctgcctgc tgtggaaacc 800
 caggccccaa ctcccttagc aacgaaagac ccgccctcca tggcaacaga 850
 ggctccacct tgcgtaacaa ctgagggtccc ttccattttg gcagctcaca 900
 gcctgcctc cttggatgag gagccagtta ccttcccaa atcgacccat 950
 gttcctatcc caaaatcagc agacaaagt acagacaaaa caaaagtgcc 1000
 ctctaggagc ccagagaact ctctggaccc caagatgtcc ctgacagggg 1050
 caagggaaact cctaccccat gcccaggagg aggctgaggc tgaggctgag 1100
 ttgcctcctt ccagttaggt cttggcctca gtttttccag cccaggacaa 1150
 gccaggtgag ctgcaggcca cactggacca cacggggcac acctcctcca 1200
 agtccctgcc caatttcccc aatacctctg ccaccgctaa tgccacgggt 1250
 gggcgtgcc tggtctgca gtcgtccttg ccagggtcag agggccctga 1300
 caagcctagc gttgtgtcag ggctgaactc gggccctggg catgtgtggg 1350
 gccctctcct gggactactg ctctgcctc ctctggtgtt ggctggaatc 1400

Lys	Thr	Glu	Arg	Ile 140	Gly	Cys	Gly	Ser	His 145	Phe	Cys	Glu	Lys	Leu 150
Gln	Gly	Val	Glu	Glu 155	Thr	Asn	Ile	Glu	Leu 160	Leu	Val	Cys	Asn	Tyr 165
Glu	Pro	Pro	Gly	Asn 170	Val	Lys	Gly	Lys	Arg 175	Pro	Tyr	Gln	Glu	Gly 180
Thr	Pro	Cys	Ser	Gln 185	Cys	Pro	Ser	Gly	Tyr 190	His	Cys	Lys	Asn	Ser 195
Leu	Cys	Glu	Pro	Ile 200	Gly	Ser	Pro	Glu	Asp 205	Ala	Gln	Asp	Leu	Pro 210
Tyr	Leu	Val	Thr	Glu 215	Ala	Pro	Ser	Phe	Arg 220	Ala	Thr	Glu	Ala	Ser 225
Asp	Ser	Arg	Lys	Met 230	Gly	Thr	Pro	Ser	Ser 235	Leu	Ala	Thr	Gly	Ile 240
Pro	Ala	Phe	Leu	Val 245	Thr	Glu	Val	Ser	Gly 250	Ser	Leu	Ala	Thr	Lys 255
Ala	Leu	Pro	Ala	Val 260	Glu	Thr	Gln	Ala	Pro 265	Thr	Ser	Leu	Ala	Thr 270
Lys	Asp	Pro	Pro	Ser 275	Met	Ala	Thr	Glu	Ala 280	Pro	Pro	Cys	Val	Thr 285
Thr	Glu	Val	Pro	Ser 290	Ile	Leu	Ala	Ala	His 295	Ser	Leu	Pro	Ser	Leu 300
Asp	Glu	Glu	Pro	Val 305	Thr	Phe	Pro	Lys	Ser 310	Thr	His	Val	Pro	Ile 315
Pro	Lys	Ser	Ala	Asp 320	Lys	Val	Thr	Asp	Lys 325	Thr	Lys	Val	Pro	Ser 330
Arg	Ser	Pro	Glu	Asn 335	Ser	Leu	Asp	Pro	Lys 340	Met	Ser	Leu	Thr	Gly 345
Ala	Arg	Glu	Leu	Leu 350	Pro	His	Ala	Gln	Glu 355	Glu	Ala	Glu	Ala	Glu 360
Ala	Glu	Leu	Pro	Pro 365	Ser	Ser	Glu	Val	Leu 370	Ala	Ser	Val	Phe	Pro 375
Ala	Gln	Asp	Lys	Pro 380	Gly	Glu	Leu	Gln	Ala 385	Thr	Leu	Asp	His	Thr 390
Gly	His	Thr	Ser	Ser 395	Lys	Ser	Leu	Pro	Asn 400	Phe	Pro	Asn	Thr	Ser 405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser
 410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser
 425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly
 440 445 450

Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe
 455 460

<210> 286

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

tcctgcagtt tcctgatgc 19

<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 288

atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45

<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

<400> 289

gtaactgaag tcaggctttt catttgggaa gccccctcaa cagaattcgg 50

tggctttgtg tgtgatgatt ttcccaaacc ccagatcacg gttcagccag 1400
 aaacacagtc ggcaataaaa ggttccaatt tgagtttcat ctgctcagct 1450
 gccagcagca gtgattcccc aatgactttt gcttggaanaa aagacaatga 1500
 actactgcat gatgctgaaa tggaaaatta tgcacacctc cgggcccag 1550
 gtggcgaggt gatggagtat accaccatcc ttgggctgctg cgaggtggaa 1600
 tttgccagtg aggggaaata tcagtgtgtc atctccaatc actttgggtc 1650
 atcctactct gtcaaagcca agcttacagt aaatatgctt cctcattca 1700
 ccaagacccc catggatctc accatccgag ctggggccat ggcacgcttg 1750
 gagtgtgctg ctgtggggca cccagcccc cagatagcct ggcagaagga 1800
 tgggggcaca gacttcccag ctgcacggga gagacgcatg catgtgatgc 1850
 ccgaggatga cgtgttcttt atcgtggatg tgaagataga ggacattggg 1900
 gtatacagct gcacagctca gaacagtgca ggaagtattt cagcaaatgc 1950
 aactctgact gtctagaaa caccatcatt tttgcgcca ctgttggaac 2000
 gaactgtaac caaggagaaa acagccgtcc tacagtgcac tgctggagga 2050
 agccctcccc ctaaactgaa ctggaccaa gatgatagcc cattggtggt 2100
 aaccgagagg cacttttttg cagcaggcaa tcagcttctg attattgtgg 2150
 actcagatgt cagtgatgct gggaaataca catgtgagat gtctaacc 2200
 cttggcactg agagaggaaa cgtgcgctc agtgtgatcc cactccaac 2250
 ctgcgactcc cctcagatga cagccccatc gttagacgat gacggatggg 2300
 cactgtggg tgctgtgatc atagccgtgg tttgctgtgt ggtgggcacg 2350
 tcaactgtgt ggggtggtcat catataccac acaaggcgga ggaatgaaga 2400
 ttgcagcatt accaacacag atgagaccaa cttgccagca gatattccta 2450
 gttatttgtc atctcaggga acgttagctg acaggcagga tgggtacgtg 2500
 tcttcagaaa gtggaagcca ccaccagttt gtcacatctt caggtgctgg 2550
 atttttctta ccacaacatg acagtagtgg gacctgcat attgacaata 2600
 gcagtgaagc tgatgtggaa gctgccacag atctgttcct ttgtccgttt 2650
 ttgggatcca caggccctat gtatttgaag ggaaatgtgt atggctcaga 2700

tccttttgaa acatatcata cagggtgcag tcctgaccca agaacagttt 2750
 taatggacca ctatgagccc agttacataa agaaaaagga gtgctaccca 2800
 tgtttctcatc cttcagaaga atcctgcgaa cggagcttca gtaatatatc 2850
 gtggccttca catgtgagga agctacttaa cactagttac tctcacaatg 2900
 aaggacctgg aatgaaaaat ctgtgtctaa acaagtcctc tttagatttt 2950
 agtgcaaate cagagccagc gtcggttgcc tcgagtaatt ctttcatggg 3000
 tacctttgga aaagctctca ggagacctca cctagatgcc tattcaagct 3050
 ttggacagcc atcagattgt cagccaagag ccttttattt gaaagctcat 3100
 tcttccccag acttggactc tgggtcagag gaagatggga aagaaaggac 3150
 agattttcag gaagaaaate acatttgtac ctttaaacag actttagaaa 3200
 actacaggac tccaaatttt cagtcttatg acttggacac atagactgaa 3250
 tgagacccaa ggaaaagctt aacatactac ctcaagtga cttttattta 3300
 aaagagagag aatcttatgt tttttaaatg gagttatgaa ttttaaagg 3350
 ataaaaatgc tttatttata cagatgaacc aaaattacaa aaagttatga 3400
 aaatttttat actgggaatg atgctcatat aagaatacct ttttaaacta 3450
 ttttttaact ttgttttatg caaaaaagta tcttacgtaa attaatgata 3500
 taaatcatga ttattttatg tatttttata atgccagatt tctttttatg 3550
 gaaaatgagt tactaaagca ttttaaataa tacctgcctt gtaccatttt 3600
 ttaaatagaa gttacttcat tatattttgc acattatatt taataaaatg 3650
 tgtcaatttg aa 3662

<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

Met	Val	Asp	Val	Leu	Leu	Leu	Phe	Ser	Leu	Cys	Leu	Leu	Phe	His
1				5					10				15	

Ile	Ser	Arg	Pro	Asp	Leu	Ser	His	Asn	Arg	Leu	Ser	Phe	Ile	Lys
				20				25					30	

Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu
				35					40					45
Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser
				50					55					60
Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu
				65					70					75
Ile	Leu	Pro	Glu	His	Leu	Lys	Glu	Phe	Gln	Ser	Leu	Glu	Thr	Leu
				80					85					90
Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro
				95					100					105
Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr
				110					115					120
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu
				125					130					135
Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys
				140					145					150
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn
				155					160					165
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala
				170					175					180
Leu	Lys	Ser	Leu	Lys	Met	Gln	Arg	Asn	Gly	Val	Thr	Lys	Leu	Met
				185					190					195
Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu
				200					205					210
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly
				215					220					225
Leu	Leu	Met	Leu	Gln	Glu	Leu	His	Leu	Ser	Gln	Asn	Ala	Ile	Asn
				230					235					240
Arg	Ile	Ser	Pro	Asp	Ala	Trp	Glu	Phe	Cys	Gln	Lys	Leu	Ser	Glu
				245					250					255
Leu	Asp	Leu	Thr	Phe	Asn	His	Leu	Ser	Arg	Leu	Asp	Asp	Ser	Ser
				260					265					270
Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn
				275					280					285
Arg	Val	Ser	Tyr	Ile	Ala	Asp	Cys	Ala	Phe	Arg	Gly	Leu	Ser	Ser

1-1000-300000

290	295	300
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile		
305	310	315
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
320	325	330
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala		
335	340	345
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
350	355	360
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys		
365	370	375
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
380	385	390
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
395	400	405
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
410	415	420
Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp		
425	430	435
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala		
440	445	450
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser		
455	460	465
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu		
470	475	480
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln		
485	490	495
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu		
500	505	510
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn		
515	520	525
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn		
530	535	540
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg		
545	550	555

Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His	Pro
560		565	570
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe	Pro
575		580	585
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp	Val
590		595	600
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr	Ser
605		610	615
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala	Thr
620		625	630
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu	Asp
635		640	645
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile	Ala
650		655	660
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp	Ser
665		670	675
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn	Gln
680		685	690
Leu Leu Ile Ile	Val Asp Ser Asp Val	Ser Asp Ala Gly Lys	Tyr
695		700	705
Thr Cys Glu Met	Ser Asn Thr Leu Gly	Thr Glu Arg Gly Asn	Val
710		715	720
Arg Leu Ser Val	Ile Pro Thr Pro Thr	Cys Asp Ser Pro Gln	Met
725		730	735
Thr Ala Pro Ser	Leu Asp Asp Asp Gly	Trp Ala Thr Val Gly	Val
740		745	750
Val Ile Ile Ala	Val Val Cys Cys Val	Val Gly Thr Ser Leu	Val
755		760	765
Trp Val Val Ile	Ile Tyr His Thr Arg	Arg Arg Asn Glu Asp	Cys
770		775	780
Ser Ile Thr Asn	Thr Asp Glu Thr Asn	Leu Pro Ala Asp Ile	Pro
785		790	795
Ser Tyr Leu Ser	Ser Gln Gly Thr Leu	Ala Asp Arg Gln Asp	Gly
800		805	810

FEET 5000

<212> DNA

<213> Homo Sapien

<400> 291

```

ggggagagga attgaccatg taaaaggaga cttttttttt tgggtggtggt 50
ggctgttggg tgccttgcaa aaatgaagga tgcaggacgc agctttctcc 100
tggaaccgaa cgcaatggat aaactgattg tgcaagagag aaggaagaac 150
gaagcttttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200
acacagggag cattcaagaa tgaaataaac cagagttaga cccgcggggg 250
ttggtgtggt ctgacataaa taaataatct taaagcagct gttccccctcc 300
ccacccccaa aaaaaaggat gattggaaat gaagaaccga ggattcacia 350
agaaaaaagt atgttcattt ttctctataa aggagaaagt gagccaagga 400
gatatttttg gaatgaaaag tttggggctt ttttagtaaa gtaaagaact 450
ggtgtggtgg tgttttcctt tctttttgaa tttcccacia gaggagagga 500
aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgcg 550
gcagattgag gcattgattg ggggagagaa accagcagag cacagttgga 600
tttgtgcta tggtgactaa aattgacgga taattgcagt tggatttttc 650
ttcatcaacc tctttttttt taaattttta ttcttttgg tatcaagatc 700
atgcgttttc tcttggtctt aaccacctgg atttccatct ggatgttgct 750
gtgatcagtc tgaaatacaa ctgtttgaat tccagaagga ccaacaccag 800
ataaattatg aatgttgaac aagatgacct tacatccaca gcagataatg 850
ataggtccta ggtttaacag ggccctattt gacccctgc ttgtggtgct 900
gctggtctct caacttcttg tgggtggtgg tctggtgcgg gctcagacct 950
gcccttctgt gtgctcctgc agcaaccagt tcagcaaggt gatttgtggt 1000
cggaaaaaac tgcgtgaggt tccggatggc atctccacca acacacggct 1050
gctgaacctc catgagaacc aaatccagat catcaaagtg aacagcttca 1100
agcacttgag gcacttgga atcctacagt tgagtaggaa ccatatcaga 1150
accattgaaa ttggggcttt caatggtctg gcgaacctca acactctgga 1200
actctttgac aatcgtctta ctaccatccc gaatggagct tttgtatact 1250

```


155										160				165			
Tyr	Ala	Phe	Asn	Arg	Ile	Pro	Ser	Leu	Arg	Arg	Leu	Asp	Leu	Gly			
				170					175					180			
Glu	Leu	Lys	Arg	Leu	Ser	Tyr	Ile	Ser	Glu	Gly	Ala	Phe	Glu	Gly			
				185					190					195			
Leu	Ser	Asn	Leu	Arg	Tyr	Leu	Asn	Leu	Ala	Met	Cys	Asn	Leu	Arg			
				200					205					210			
Glu	Ile	Pro	Asn	Leu	Thr	Pro	Leu	Ile	Lys	Leu	Asp	Glu	Leu	Asp			
				215					220					225			
Leu	Ser	Gly	Asn	His	Leu	Ser	Ala	Ile	Arg	Pro	Gly	Ser	Phe	Gln			
				230					235					240			
Gly	Leu	Met	His	Leu	Gln	Lys	Leu	Trp	Met	Ile	Gln	Ser	Gln	Ile			
				245					250					255			
Gln	Val	Ile	Glu	Arg	Asn	Ala	Phe	Asp	Asn	Leu	Gln	Ser	Leu	Val			
				260					265					270			
Glu	Ile	Asn	Leu	Ala	His	Asn	Asn	Leu	Thr	Leu	Leu	Pro	His	Asp			
				275					280					285			
Leu	Phe	Thr	Pro	Leu	His	His	Leu	Glu	Arg	Ile	His	Leu	His	His			
				290					295					300			
Asn	Pro	Trp	Asn	Cys	Asn	Cys	Asp	Ile	Leu	Trp	Leu	Ser	Trp	Trp			
				305					310					315			
Ile	Lys	Asp	Met	Ala	Pro	Ser	Asn	Thr	Ala	Cys	Cys	Ala	Arg	Cys			
				320					325					330			
Asn	Thr	Pro	Pro	Asn	Leu	Lys	Gly	Arg	Tyr	Ile	Gly	Glu	Leu	Asp			
				335					340					345			
Gln	Asn	Tyr	Phe	Thr	Cys	Tyr	Ala	Pro	Val	Ile	Val	Glu	Pro	Pro			
				350					355					360			
Ala	Asp	Leu	Asn	Val	Thr	Glu	Gly	Met	Ala	Ala	Glu	Leu	Lys	Cys			
				365					370					375			
Arg	Ala	Ser	Thr	Ser	Leu	Thr	Ser	Val	Ser	Trp	Ile	Thr	Pro	Asn			
				380					385					390			
Gly	Thr	Val	Met	Thr	His	Gly	Ala	Tyr	Lys	Val	Arg	Ile	Ala	Val			
				395					400					405			
Leu	Ser	Asp	Gly	Thr	Leu	Asn	Phe	Thr	Asn	Val	Thr	Val	Gln	Asp			
				410					415					420			

P
 E
 P
 T
 E
 R
 S
 E
 R
 I
 E
 S
 O
 F
 A
 M
 I
 L
 I
 A
 R
 E
 S
 I
 N
 T
 H
 E
 S
 E
 S
 E
 C
 T
 I
 O
 N
 S

```
<210> 293
<211> 4053
<212> DNA

<213> Homo Sapien

<400> 293
agccgacgct gctcaagctg caactctggt gcagttggca gttcttttcg 50
```


gtttccctcc tgetgtttgg gggcatgaaa gggcttcgcc gccgggagta 100
 aaagaaggaa ttgaccgggc agcgcgaggg aggagcgcgc acgcgaccgc 150
 gagggcgggc gtgcaccctc ggctggaagt ttgtgccggg ccccgagcgc 200
 gcgcgggctg ggagcttcgg gtagagacct aggccgctgg accgcgatga 250
 gcgcgcgag cctccgtgcg cgcgcgcgg ggttggggct gctgctgtgc 300
 gcggtgctgg ggcgcgctgg ccggtccgac agcggcggtc gcggggaact 350
 cgggcagccc tctggggtag ccgcgagcg cccatgcccc actacctgcc 400
 gctgcctcgg ggacctgctg gactgcagtc gtaagcggct agcgcgtctt 450
 cccgagccac tcccgctctg ggtcgctcgg ctggacttaa gtcacaacag 500
 attatctttc atcaaggcaa gttccatgag ccaccttcaa agccttcgag 550
 aagtgaact gaacaacaat gaattggaga ccattccaaa tctgggacca 600
 gtctcgcaa atattacact tctctccttg gctggaaaca ggattgttga 650
 aatactccct gaacatctga aagagtttca gtcccttgaa actttggacc 700
 ttagcagcaa caatatttca gagctccaaa ctgcatttcc agccctacag 750
 ctcaaatac tgtatctcaa cagcaaccga gtcacatcaa tggaacctgg 800
 gtattttgac aatttgcca acacactcct tgtgttaaag ctgaacagga 850
 accgaatctc agctatccca cccaagatgt ttaaactgcc ccaactgcaa 900
 catctogaat tgaaccgaaa caagattaaa aatgtagatg gactgacatt 950
 ccaaggcctt ggtgctctga agtctctgaa aatgcaaaga aatggagtaa 1000
 cgaaacttat ggatggagct ttttgggggc tgagcaacat ggaaattttg 1050
 cagctggacc ataacaacct aacagagatt accaaaaggct ggctttacgg 1100
 cttgctgatg ctgcaggaac ttcattctcag ccaaaatgcc atcaacagga 1150
 tcagccctga tgccctgggag ttctgccaga agctcagtga gctggaccta 1200
 actttcaatc acttatcaag gttagatgat tcaagcttcc ttggcctaag 1250
 cttactaaat aactgcaca ttgggaacaa cagagtcagc tacattgctg 1300
 attgtgcctt ccgggggctt tccagtttaa agactttgga tctgaagaac 1350

gtggtgggca cgtcactcgt gtgggtgggc atcatatacc acacaaggcg 2750
 gaggaatgaa gattgcagca ttaccaaacac agatgagacc aacttgccag 2800
 cagatatcc tagttatttg tcatctcagg gaacgtagc tgacaggcag 2850
 gatgggtacg tgtcttcaga aagtggaagc caccaccagt ttgtcacatc 2900
 ttcaggtgct ggatTTTTCT taccacaaca tgacagtagt gggacctgcc 2950
 atattgacaa tagcagtga gctgatgtgg aagctgccac agatctgttc 3000
 ctttgtccgt ttttgggatc cacaggccct atgtatttga agggaaatgt 3050
 gtatggctca gatccttttg aaacatatca tacaggttgc agtcctgacc 3100
 caagaacagt tttaatggac cactatgagc ccagttacat aaagaaaaag 3150
 gagtgtacc catgttctca tccttcagaa gaatcctgcg aacggagctt 3200
 cagtaatata tcgtggcctt cacatgtgag gaagctactt aacactagtt 3250
 actctcacia tgaaggacct ggaatgaaaa atctgtgtct aaacaagtcc 3300
 tcttttagatt ttagtgcaaa tccagagcca gcgtcggttg cctcgagtaa 3350
 ttctttcatg ggtacctttg gaaaagctct caggagacct cacctagatg 3400
 cctattcaag ctttggacag ccatcagatt gtcagccaag agccttttat 3450
 ttgaaagctc attcttcccc agacttggac tctgggtcag aggaagatgg 3500
 gaaagaaagg acagattttc aggaagaaaa tcacatttgt acctttaaac 3550
 agactttaga aaactacagg actccaaatt ttcagtctta tgacttggac 3600
 acatagactg aatgagacca aaggaaaagc ttaacatact acctcaagtg 3650
 aacttttatt taaaagagag agaactttat gttttttaaa tggagttagt 3700
 aattttaaaa ggataaaaat gctttattta tacagatgaa ccaaaattac 3750
 aaaaagttat gaaaattttt atactgggaa tgatgctcat ataagaatac 3800
 ctttttaaac tattttttta ctttgtttta tgcaaaaaag tatcttacgt 3850
 aaattaatga tataaatcat gattatttta tgtattttta taatgccaga 3900
 tttcttttta tggaaaatga gttactaaag cattttaaat aatacctgcc 3950
 ttgtaccatt ttttaaatag aagttacttc atttatatttt gcacattata 4000

	215		220		225
Lys Ile Lys Asn Val Asp Gly Leu Thr	Phe Gln Gly Leu Gly Ala				
230	235				240
Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met					
245	250				255
Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu					
260	265				270
Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly					
275	280				285
Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn					
290	295				300
Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu					
305	310				315
Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser					
320	325				330
Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn					
335	340				345
Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser					
350	355				360
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile					
365	370				375
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg					
380	385				390
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala					
395	400				405
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn					
410	415				420
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys					
425	430				435
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys					
440	445				450
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln					
455	460				465
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly					
470	475				480

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

Arg Ser Ile Phe	Ala Val Ser Pro Asp	Gly Phe Val Cys Asp Asp
485		490 495
Phe Pro Lys Pro	Gln Ile Thr Val Gln	Pro Glu Thr Gln Ser Ala
500		505 510
Ile Lys Gly Ser	Asn Leu Ser Phe Ile	Cys Ser Ala Ala Ser Ser
515		520 525
Ser Asp Ser Pro	Met Thr Phe Ala Trp	Lys Lys Asp Asn Glu Leu
530		535 540
Leu His Asp Ala	Glu Met Glu Asn Tyr	Ala His Leu Arg Ala Gln
545		550 555
Gly Gly Glu Val	Met Glu Tyr Thr Thr	Ile Leu Arg Leu Arg Glu
560		565 570
Val Glu Phe Ala	Ser Glu Gly Lys Tyr	Gln Cys Val Ile Ser Asn
575		580 585
His Phe Gly Ser	Ser Tyr Ser Val Lys	Ala Lys Leu Thr Val Asn
590		595 600
Met Leu Pro Ser	Phe Thr Lys Thr Pro	Met Asp Leu Thr Ile Arg
605		610 615
Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His Pro
620		625 630
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe Pro
635		640 645
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp Val
650		655 660
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr Ser
665		670 675
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala Thr
680		685 690
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu Asp
695		700 705
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile Ala
710		715 720
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp Ser
725		730 735
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn Gln
740		745 750

485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750

Leu	Leu	Ile	Ile	Val	Asp	Ser	Asp	Val	Ser	Asp	Ala	Gly	Lys	Tyr	755	760	765
Thr	Cys	Glu	Met	Ser	Asn	Thr	Leu	Gly	Thr	Glu	Arg	Gly	Asn	Val	770	775	780
Arg	Leu	Ser	Val	Ile	Pro	Thr	Pro	Thr	Cys	Asp	Ser	Pro	Gln	Met	785	790	795
Thr	Ala	Pro	Ser	Leu	Asp	Asp	Asp	Gly	Trp	Ala	Thr	Val	Gly	Val	800	805	810
Val	Ile	Ile	Ala	Val	Val	Cys	Cys	Val	Val	Gly	Thr	Ser	Leu	Val	815	820	825
Trp	Val	Val	Ile	Ile	Tyr	His	Thr	Arg	Arg	Arg	Asn	Glu	Asp	Cys	830	835	840
Ser	Ile	Thr	Asn	Thr	Asp	Glu	Thr	Asn	Leu	Pro	Ala	Asp	Ile	Pro	845	850	855
Ser	Tyr	Leu	Ser	Ser	Gln	Gly	Thr	Leu	Ala	Asp	Arg	Gln	Asp	Gly	860	865	870
Tyr	Val	Ser	Ser	Glu	Ser	Gly	Ser	His	His	Gln	Phe	Val	Thr	Ser	875	880	885
Ser	Gly	Ala	Gly	Phe	Phe	Leu	Pro	Gln	His	Asp	Ser	Ser	Gly	Thr	890	895	900
Cys	His	Ile	Asp	Asn	Ser	Ser	Glu	Ala	Asp	Val	Glu	Ala	Ala	Thr	905	910	915
Asp	Leu	Phe	Leu	Cys	Pro	Phe	Leu	Gly	Ser	Thr	Gly	Pro	Met	Tyr	920	925	930
Leu	Lys	Gly	Asn	Val	Tyr	Gly	Ser	Asp	Pro	Phe	Glu	Thr	Tyr	His	935	940	945
Thr	Gly	Cys	Ser	Pro	Asp	Pro	Arg	Thr	Val	Leu	Met	Asp	His	Tyr	950	955	960
Glu	Pro	Ser	Tyr	Ile	Lys	Lys	Lys	Glu	Cys	Tyr	Pro	Cys	Ser	His	965	970	975
Pro	Ser	Glu	Glu	Ser	Cys	Glu	Arg	Ser	Phe	Ser	Asn	Ile	Ser	Trp	980	985	990
Pro	Ser	His	Val	Arg	Lys	Leu	Leu	Asn	Thr	Ser	Tyr	Ser	His	Asn	995	1000	1005
Glu	Gly	Pro	Gly	Met	Lys	Asn	Leu	Cys	Leu	Asn	Lys	Ser	Ser	Leu			

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

1010	1015	1020
Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn		
1025	1030	1035
Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu		
1040	1045	1050
Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg		
1055	1060	1065
Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly		
1070	1075	1080
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn		
1085	1090	1095
His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro		
1100	1105	1110
Asn Phe Gln Ser Tyr Asp Leu Asp Thr		
1115		

<210> 295

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 295

ggaaccgaat ctcagcta 18

<210> 296

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 296

cctaaactga actggacca 19

<210> 297

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 297
ggctggagac actgaacct 19

<210> 298
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 298
acagctgcac agctcagaac agtg 24

<210> 299

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 299
cattcccagt ataaaaattt tc 22

<210> 300
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 300
gggtcttggt gaatgagg 18

<210> 301
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 301
gtgcctctcg gttaccacca atgg 24

<210> 302
<211> 50
<212> DNA
<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

gcggccactg ttggaccgaa ctgtaaccaa gggagaaaca gccgtcctac 50

<211> 28

<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

gcctttgaca accttcagtc actagtgg 28

<211> 24

<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

cccatgtgt ccatgactgt tccc 24

<211> 45

<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

tactgcctca tgacctcttc actcccttgc atcatcttag agcgg 45

<211> 24

<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

actccaagga aatcggatcc gttc 24

<211> 24

atctgactcg gcacccctg caggcaccat ggcccagagc cgggtgctgc 450
 tgctcctgct gctgctgccg ccacagctgc acctgggacc tgtgcttgcc 500
 gtgagggccc caggatttgg ccgaagtggc ggccacagcc tgagccccga 550
 agagaacgaa tttgctggagg aggagccggt gctggtactg agccctgagg 600
 agcccggggc tggcccagcc gcggtcagct gcccgcgaga ctgtgctgt 650
 tcccaggagg gcgtcgtgga ctgtggcggt attgacctgc gtgagttccc 700
 gggggacctg cctgagcaca ccaaccacct atctctgcag aacaaccage 750
 tggaaaagat ctacctgag gagctctccc ggctgcaccg gctggagaca 800
 ctgaacctgc aaaacaaccg cctgacttcc cgagggctcc cagagaaggc 850
 gtttgagcat ctgaccaacc tcaattacct gtacttggcc aataacaagc 900
 tgaccttgcc accccgcttc ctgccaaacg cctgatcag tgtggacttt 950
 gctgccaaact atctcaccaa gatctatggg ctacactttg gccagaagcc 1000
 aaacttgagg tctgtgtacc tgcacaacaa caagctggca gacgccgggc 1050
 tgccggacaa catgttcaac ggctccagca acgtcgaggt cctcatcctg 1100
 tccagcaact tctgcgcca cgtgcccaag cacctgcgc ctgccctgta 1150
 caagctgcac ctcaagaaca acaagctgga gaagatcccc ccgggggacct 1200
 tcagcgagct gagcagcctg cgcgagctat acctgcagaa caactacctg 1250
 actgacgagg gcctggacaa cgagaccttc tggaagctct ccagcctgga 1300
 gtacctggat ctgtccagca acaacctgtc tgggtccca gctgggctgc 1350
 cgcgcagcct ggtgctgctg cacttgagga agaacgccat ccggagcgtg 1400
 gacgcgaatg tgctgacccc catccgcagc ctggagtacc tgctgctgca 1450
 cagcaaccag ctgcgggagc agggcatcca cccactggcc ttccagggcc 1500
 tcaagcggtt gcacacggtg cacctgtaca acaacgcgt ggagcgcgtg 1550
 cccagtggcc tgctcgcgc cgtgcgcacc ctcatgatcc tgcacaacca 1600
 gatcacaggc attggccgcg aagactttgc caccacctac ttctggagg 1650
 agctcaacct cagctacaac cgcatacca gccacaggt gcaccgcgac 1700

[illegible]

cctgggtgct gctggggcct tggggcagga gtgaagcaga ggtgatgggg 3100
 ctgggctgag ccagggagga aggaccagc tgcacctagg agacaccttt 3150
 gttcttcagg cctgtggggg aagttccggg tgcctttatt ttttattctt 3200
 ttctaaggaa aaaaatgata aaaatctcaa agctgatttt tcttggtata 3250
 gaaaaactaa tataaaagca ttatccctat ccctgcaaaa aaaaaa 3296

<210> 311

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 311

gcattggccg cgagactttg cc 22

<210> 312

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 312

gcggccacgg tccttggaat tg 22

<210> 313

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 313

tggaggagct caacctcagc tacaaccgca tcaccagccc acagg 45

<210> 314

<211> 3003

<212> DNA

<213> Homo Sapien

<400> 314

gggagggggc tccggggcgc gcgcagcaga cctgctccgg ccgcgcgcct 50

cgccgctgtc ctccggggagc ggcagcagta gcccgggcgg cgagggctgg 100

ggggttcctcg agactctcag aggggcgccct cccatcggcg cccaccaccc 150
 caacctgttc ctgcgcgcgc actgcgctgc gcccaggac ccgctgcca 200
 acatggattt tctcctggcg ctggtgctgg tctcctcgt ctacctgcag 250
 gcggccgcgc agttcgacgg gaggtggccc aggcaaatag tgtcatcgat 300
 tggcctatgt cgttatggtg ggaggattga ctgctgctgg ggctgggctc 350
 gccagtcttg gggacagtgt cagcctgtgt gccaccacg atgcaaacaat 400
 ggtgaatgta tcggggccaaa caagtgcag tgctatcctg gttatgctgg 450
 aaaaacctgt aatcaagatc taaatgagtg tggcctgaag ccccgccct 500
 gtaagcacag gtgcatgaac acttacggca gctacaagtg ctactgtctc 550
 aacggatata tgctcatgcc ggatgggtcc tgctcaagtg ccctgacctg 600
 ctccatggca aactgtcagt atggctgtga tgttgtaaa ggacaaatac 650
 ggtgccagtg cccatccct ggctgcacc tggctcctga tgggaggacc 700
 tgtgtagatg ttgatgaatg tgctacagga agagcctcct gccctagatt 750
 taggcaatgt gtcaacactt ttgggagcta catctgcaag tgctataaag 800
 gcttcgatct catgtatatt ggaggcaaat atcaatgtca tgacatagac 850
 gaatgtcac ttggtcagta tcagtgcagc agctttgctc gatgttataa 900
 cgtacgtggg tcctacaagt gcaaatgtaa agaaggatac cagggtgatg 950
 gactgacttg tgtgtatata ccaaaagtta tgattgaacc ttcaggcca 1000
 attcatgtac caaagggaaa tgggtaccatt ttaaagggtg acacaggaaa 1050
 taataattgg attcctgatg ttggaagtac ttggtggcct ccgaagacac 1100
 catatattcc tcctatcatt accaacaggc ctacttctaa gccacaaca 1150
 agacctacac caaagccaac accaattcct actccaccac caccaccacc 1200
 cctgccaca gagctcagaa cacctctacc acctacaacc ccagaaaggc 1250
 caaccaccgg actgacaact atagcaccag ctgccagtac acctccagga 1300
 gggattacag ttgacaacag ggtacagaca gaccctcaga aaccagagg 1350
 agatgtgttc agtgttctgg tacacagttg taattttgac catggacttt 1400

gtggatggat cagggagaaa gacaatgact tgcaactggga accaatcagg 1450
 gaccagcag gtggacaata tctgacagtg tcggcagcca aagccccagg 1500
 gggaaaagct gcacgcttgg tgetacctct eggccgcctc atgcattcag 1550
 gggacctgtg cctgtcattc aggcacaagg tgacggggct gcactctggc 1600
 aactccagg tgtttgtgag aaaacacggt gccacaggag cagccctgtg 1650
 gggaagaaat ggtggccatg gctggaggca aacacagatc accttgcgag 1700
 gggctgacat caagagcgaa tcacaaagat gattaaagg ttggaaaaaa 1750
 agatctatga tggaaaatta aaggaactgg gattattgag cctggagaag 1800
 agaagactga ggggcaaacc attgatgggt ttcaagtata tgaagggttg 1850
 gcacagagag ggtggcgacc agctgttctc catatgcact aagaatagaa 1900
 caagaggaaa ctggcttaga ctagagtata agggagcatt tcttggcagg 1950
 ggccattgtt agaatacttc ataaaaaaag aagtgtgaaa atctcagtat 2000
 ctctctctct ttctaaaaaa ttagataaaa atttgtctat ttaagatggg 2050
 taaagatggt cttacccaag gaaaagtaac aaattataga atttcccaa 2100
 agatgttttg atcctactag tagtatgcag tgaaaatctt tagaactaaa 2150
 taatttgac aaggettaat ttaggcattt cctcttgac ctctaattgg 2200
 agagggattg aaaggggaag agcccaccaa atgctgagct cactgaaata 2250
 tctctccctt atggcaatcc tagcagtatt aaagaaaaaa ggaaactatt 2300
 tattccaaat gagagtatga tggacagata ttttagtatc tcagtaatgt 2350
 cctagtgtgg cgggtgtttt caatgtttct tcatggtaaa ggtataagcc 2400
 tttcatttgt tcaatggatg atgtttcaga tttttttttt ttaagagat 2450
 cttcaagga acacagttca gagagatttt catcgggtgc attctctctg 2500
 cttcgtgtgt gacaagttat cttggctgct gagaaagagt gccctgcccc 2550
 acaccggcag acctttcctt cacctcatca gtatgattca gtttctctta 2600
 tcaattggac tctcccagg tccacagaac agtaatat tttgaacaat 2650
 aggtacaata gaaggtcttc tgtcatttaa cctggtaaag gcagggctgg 2700
 agggggaaaa taaatcatta agcctttgag taacggcaga atatatggct 2750

Thr Cys Val Asp	Val Asp Glu Cys Ala	Thr Gly Arg Ala Ser Cys
170		175 180
Pro Arg Phe Arg	Gln Cys Val Asn Thr	Phe Gly Ser Tyr Ile Cys
185		190 195
Lys Cys His Lys	Gly Phe Asp Leu Met	Tyr Ile Gly Gly Lys Tyr
200		205 210
Gln Cys His Asp	Ile Asp Glu Cys Ser	Leu Gly Gln Tyr Gln Cys
215		220 225
Ser Ser Phe Ala	Arg Cys Tyr Asn Val	Arg Gly Ser Tyr Lys Cys
230		235 240
Lys Cys Lys Glu	Gly Tyr Gln Gly Asp	Gly Leu Thr Cys Val Tyr
245		250 255
Ile Pro Lys Val	Met Ile Glu Pro Ser	Gly Pro Ile His Val Pro
260		265 270
Lys Gly Asn Gly	Thr Ile Leu Lys Gly	Asp Thr Gly Asn Asn Asn
275		280 285
Trp Ile Pro Asp	Val Gly Ser Thr Trp	Trp Pro Pro Lys Thr Pro
290		295 300
Tyr Ile Pro Pro	Ile Ile Thr Asn Arg	Pro Thr Ser Lys Pro Thr
305		310 315
Thr Arg Pro Thr	Pro Lys Pro Thr Pro	Ile Pro Thr Pro Pro Pro
320		325 330
Pro Pro Pro Leu	Pro Thr Glu Leu Arg	Thr Pro Leu Pro Pro Thr
335		340 345
Thr Pro Glu Arg	Pro Thr Thr Gly Leu	Thr Thr Ile Ala Pro Ala
350		355 360
Ala Ser Thr Pro	Pro Gly Gly Ile Thr	Val Asp Asn Arg Val Gln
365		370 375
Thr Asp Pro Gln	Lys Pro Arg Gly Asp	Val Phe Ser Val Leu Val
380		385 390
His Ser Cys Asn	Phe Asp His Gly Leu	Cys Gly Trp Ile Arg Glu
395		400 405
Lys Asp Asn Asp	Leu His Trp Glu Pro	Ile Arg Asp Pro Ala Gly
410		415 420
Gly Gln Tyr Leu	Thr Val Ser Ala Ala	Lys Ala Pro Gly Gly Lys

THE "BIOLOGICAL"

	425		430		435
Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly					
	440		445		450
Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser					
	455		460		465
Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala					
	470		475		480
Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln					
	485		490		495
Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg					
	500		505		

<210> 316
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 316
 gatggttcct gctcaagtgc cctg 24

<210> 317
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 317
 ttgcacttgt aggacccacg tacg 24

<210> 318
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 318
 ctgatgggag gacctgtgta gatgttgatg aatgtgctac aggaagagcc 50

<210> 319
 <211> 2110
 <212> DNA

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

<213> Homo Sapien

<400> 319

```

cttctttgaa aaggattatc acctgatcag gttctctctg catttgcccc 50
tttagattgt gaaatgtggc tcaaggtctt cacaactttc ctttcctttg 100
caacaggtgc ttgctcgggg ctgaaggtga cagtgccatc acacactgtc 150
catggcgctca gaggtcaggc cctctaccta cccgtccact atggcttcca 200
cactccagca tcagacatcc agatcatatg gctatttgag agaccccaca 250
caatgcccaa atacttactg ggctctgtga ataagtctgt ggttcctgac 300
ttggaatacc aacacaagtt caccatgatg ccaccaatg catctctgct 350
tatcaaccca ctgcagttcc ctgatgaagg caattacatc gtgaaggtca 400
acattcaggg aaatggaact ctatctgccg gtcagaagat acaagtcacg 450
gttgatgatc ctgtcacaaa gccagtggtg cagattcatc ctccctctgg 500
ggctgtggag tatgtgggga acatgacct gacatgccat gtggaagggg 550
gcactcggct agcttaccaa tggctaaaaa atgggagacc tgtccacacc 600
agctccacct actccttttc tccccaaaac aatacccttc atattgctcc 650
agtaaccaag gaagacattg ggaattacag ctgcctgggtg aggaaccctg 700
tcagtgaat ggaaagtgat atcattatgc ccatcatata ttatggacct 750
tatggacttc aagtgaattc tgataaaggg ctaaaagtag ggggaagtgtt 800
tactgttgac cttggagagg ccacacctatt tgattgttct gctgattctc 850
atccccccaa cacctactcc tggattagga ggactgacaa tactacatat 900
atcattaagc atgggcctcg cttagaagtt gcactctgaga aagtagccca 950
gaagacaatg gactatgtgt gctgtgctta caacaacata accggcaggc 1000
aagatgaaac tcatttcaca gttatcatca cttccgtagg actggagaag 1050
cttgacaga aaggaaaatc attgtcacct ttagcaagta taactggaat 1100
atcactatct ttgattatat ccatgtgtct tctcttcta tggaaaaaat 1150
atcaacccta caaagttata aaacagaaac tagaaggcag gccagaaaca 1200
gaatacagga aagctcaaac attttcaggc catgaagatg ctctggatga 1250

```


Pro	His	Thr	Met	Pro	Lys	Tyr	Leu	Leu	Gly	Ser	Val	Asn	Lys	Ser	
				65					70					75	
Val	Val	Pro	Asp	Leu	Glu	Tyr	Gln	His	Lys	Phe	Thr	Met	Met	Pro	
				80					85					90	
Pro	Asn	Ala	Ser	Leu	Leu	Ile	Asn	Pro	Leu	Gln	Phe	Pro	Asp	Glu	
				95					100					105	
Gly	Asn	Tyr	Ile	Val	Lys	Val	Asn	Ile	Gln	Gly	Asn	Gly	Thr	Leu	
				110					115					120	
Ser	Ala	Ser	Gln	Lys	Ile	Gln	Val	Thr	Val	Asp	Asp	Pro	Val	Thr	
				125					130					135	
Lys	Pro	Val	Val	Gln	Ile	His	Pro	Pro	Ser	Gly	Ala	Val	Glu	Tyr	
				140					145					150	
Val	Gly	Asn	Met	Thr	Leu	Thr	Cys	His	Val	Glu	Gly	Gly	Thr	Arg	
				155					160					165	
Leu	Ala	Tyr	Gln	Trp	Leu	Lys	Asn	Gly	Arg	Pro	Val	His	Thr	Ser	
				170					175					180	
Ser	Thr	Tyr	Ser	Phe	Ser	Pro	Gln	Asn	Asn	Thr	Leu	His	Ile	Ala	
				185					190					195	
Pro	Val	Thr	Lys	Glu	Asp	Ile	Gly	Asn	Tyr	Ser	Cys	Leu	Val	Arg	
				200					205					210	
Asn	Pro	Val	Ser	Glu	Met	Glu	Ser	Asp	Ile	Ile	Met	Pro	Ile	Ile	
				215					220					225	
Tyr	Tyr	Gly	Pro	Tyr	Gly	Leu	Gln	Val	Asn	Ser	Asp	Lys	Gly	Leu	
				230					235					240	
Lys	Val	Gly	Glu	Val	Phe	Thr	Val	Asp	Leu	Gly	Glu	Ala	Ile	Leu	
				245					250					255	
Phe	Asp	Cys	Ser	Ala	Asp	Ser	His	Pro	Pro	Asn	Thr	Tyr	Ser	Trp	
				260					265					270	
Ile	Arg	Arg	Thr	Asp	Asn	Thr	Thr	Tyr	Ile	Ile	Lys	His	Gly	Pro	
				275					280					285	
Arg	Leu	Glu	Val	Ala	Ser	Glu	Lys	Val	Ala	Gln	Lys	Thr	Met	Asp	
				290					295					300	
Tyr	Val	Cys	Cys	Ala	Tyr	Asn	Asn	Ile	Thr	Gly	Arg	Gln	Asp	Glu	
				305					310					315	
Thr	His	Phe	Thr	Val	Ile	Ile	Thr	Ser	Val	Gly	Leu	Glu	Lys	Leu	

```
<210> 321
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 321
gatcctgtca caaagccagt ggtgc 25

<210> 322

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 322
cactgacagg gttcctcacc cagg 24

<210> 323
<211> 45
<212> DNA
<213> Artificial Sequence
```

<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

ctccctctgg gctgtggagt atgtggggaa catgaccctg acatg 45

<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

gcaagcggcg aaatggcgcc ctccgggagt cttgcagttc ccctggcagt 50
 cctgggtgctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100
 acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150
 tggatgatag aattttatgc cccgtgggtgc cctgcttgctc aaaatcttca 200
 accggaatgg gaaagttttg ctgaatgggg agaagatctt gaggttaata 250
 ttgcgaaagt agatgtcaca gagcagccag gactgagtgg acggttttatc 300
 ataactgctc ttctactat ttatcattgt aaagatgggtg aatttaggcg 350
 ctatcagggt ccaaggacta agaaggactt cataaacttt ataagtgata 400
 aagagtggaa gagtattgag cccgtttcat catggtttgg tccaggttct 450
 gttctgatga gtagtatgtc agcactcttt cagctatcta tgtggatcag 500
 gacgtgccat aactacttta ttgaagacct tggattgcca gtgtggggat 550
 catatactgt ttttgcttta gcaactctgt tttccggact gttattagga 600
 ctctgtatga tatttggtggc agattgcctt tgtccttcaa aaaggcgcag 650
 accacagcca taccataacc cttcaaaaaa attattatca gaatctgcac 700
 aacctttgaa aaaagtggag gaggaacaag aggcggatga agaagatgtt 750
 tcagaagaag aagctgaaag taaagaagga acaaacaaag actttccaca 800
 gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850
 cctagttaaa ttttatagtt atcttaatat tatgatTTTT ataaaaacag 900
 aagattgatc attttgTTTT gtttgaagtg aactgtgact tttttgaata 950
 ttgcagggtt cagtctagat tgtcattaaa ttgaagagtc tacattcaga 1000

2397
 2398
 2399
 2400
 2401
 2402
 2403
 2404
 2405
 2406
 2407
 2408
 2409
 2410
 2411
 2412
 2413
 2414
 2415
 2416
 2417
 2418
 2419
 2420
 2421
 2422
 2423
 2424
 2425
 2426
 2427
 2428
 2429
 2430
 2431
 2432
 2433
 2434
 2435
 2436
 2437
 2438
 2439
 2440
 2441
 2442
 2443
 2444
 2445
 2446
 2447
 2448
 2449
 2450
 2451
 2452
 2453
 2454
 2455
 2456
 2457
 2458
 2459
 2460
 2461
 2462
 2463
 2464
 2465
 2466
 2467
 2468
 2469
 2470
 2471
 2472
 2473
 2474
 2475
 2476
 2477
 2478
 2479
 2480
 2481
 2482
 2483
 2484
 2485
 2486
 2487
 2488
 2489
 2490
 2491
 2492
 2493
 2494
 2495
 2496
 2497
 2498
 2499
 2500

215	220	225
Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu		
230	235	240
Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu		
245	250	255
Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser		
260	265	270
Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser		
275	280	

<210> 326

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 326

tgaggtgggc aagcggcgaa atg 23

<210> 327

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 327

tatgtggatc aggacgtgcc 20

<210> 328

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 328

tgcagggttc agtctagatt g 21

<210> 329

<211> 25

<212> DNA

<213> Artificial Sequence

F E E " S E T O O O

```
<400> 331
gcgagtgtcc agctgcggag acccgtgata attcgttaac taattcaaca 50
aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taaccacagt 100
ggacaggcgg attggaagag cggaaggtc ctggcccaga gcagtgtgac 150
acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200
ggtttggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250
cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300
agagtacatc cttgtggagg aagccaagct ttccaagatt aagagctggg 350
ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400
tacctggctc accctgtgaa tgctacaaa ctggtgaagc ggctaaacac 450
agactggcct gcgctggagg accttgtcct gcaggactca gctgcaggtt 500
ttatcgccaa cctctctgtg cagcggcagt tcttccccac tgatgaggac 550
gagataggag ctgccaaagc cctgatgaga cttcaggaca catacaggct 600
ggaccacaggc acaatttcca gaggggaact tccaggaacc aagtaccagg 650
caatgctgag tgtggatgac tgctttggga tgggccgctc ggccataaat 700
gaaggggact attatcatc ggtgttgtgg atggagcagg tgctaaagca 750
```

[illegible]

Asp Tyr Leu Ser	Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg	215	220	225
Ala Leu Glu Leu	Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His	230	235	240
Glu Arg Ala Gly	Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu	245	250	255
Glu Glu Arg Glu	Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu	260	265	270
Ala Thr Pro Glu	Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro	275	280	285
Glu Arg Asp Val	Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys	290	295	300
Leu Thr Pro Arg	Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His	305	310	315
Gly Asn Arg Ala	Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu	320	325	330
Asp Glu Trp Asp	Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met	335	340	345
Ser Asp Glu Glu	Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys	350	355	360
Leu Ala Arg Ala	Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr	365	370	375
Val Ala Ser Tyr	Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp	380	385	390
Asp Asp Pro Val	Val Ala Arg Val Asn Arg Arg Met Gln His Ile	395	400	405
Thr Gly Leu Thr	Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn	410	415	420
Tyr Gly Val Gly	Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg	425	430	435
Arg Pro Phe Asp	Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala	440	445	450
Thr Phe Leu Asn	Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr	455	460	465
Val Phe Pro Asp	Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr	470	475	480

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

<220>
<223> Synthetic Oligonucleotide Probe

<400> 336
acactcagca ttgcctggta cttg 24

<210> 337

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 337

gggcacatga ctgacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338

<211> 2789

<212> DNA

<213> Homo Sapien

<400> 338

gcagtattga gttttacttc ctctcttttt tagtggaaga cagaccataa 50
tcccagtgtg agtgaaattg attgtttcat ttattaccgt tttggctggg 100
ggtagttagtcc gacaccttca cagttgaaga gcaggcagaa ggagttgtga 150
agacaggaca atcttcttgg ggatgctggg cctggaagcc agcgggcctt 200
gctctgtctt tggcctcatt gaccccaggt tctctgggta aaactgaaag 250
cctactactg gcctgggtgcc catcaatcca ttgatccttg aggctgtgcc 300
cctggggcac ccacctggca gggcctacca ccatgcgact gagctccctg 350
ttggctctgc tgcggccagc gcttcccctc atcttagggc tgtctctggg 400
gtgcagcctg agcctcctgc gggtttctctg gatccagggg gagggagaag 450
atccctgtgt cgaggctgta ggggagcgag gagggccaca gaatccagat 500
tcgagagctc ggctagacca aagtgatgaa gacttcaaac cccggattgt 550
cccctactac agggacccca acaagcccta caagaaggtg ctcaggactc 600
ggtagatcca gacagagctg ggctcccgtg agcgggttgct ggtggctgtc 650
ctgacctccc gagctacact gtccactttg gccgtggctg tgaaccgtac 700
ggtggcccat cacttccctc ggttactcta cttcactggg cagcgggggg 750
cccgggctcc agcagggatg caggtgggtgt ctcattgggga tgagcggccc 800

gcctggctca tgtcagagac cctgcgccac cttcacacac actttggggc 850
 cgactacgac tggttcttca tcatgcagga tgacacatat gtgcaggccc 900
 cccgcctggc agcccttget ggccacctca gcatcaacca agacctgtac 950
 ttagggccggg cagaggagtt cattggcgca ggcgagcagg cccggtactg 1000
 tcatgggggc tttggctacc tgttgtcacg gagtctcctg cttcgtctgc 1050
 ggccacatct ggatggctgc cgaggagaca ttctcagtgc ccgtcctgac 1100
 gagtggcttg gacgtgcct cattgactct ctgggcgtcg gctgtgtctc 1150
 acagcaccag gggcagcagt atcgctcatt tgaactggcc aaaaataggg 1200
 accctgagaa ggaagggagc tcggctttcc tgagtgcctt cgcctgcac 1250
 cctgtctccg aaggtaccct catgtaccgg ctccacaaac gcttcagcgc 1300
 tctggagttg gagcgggctt acagtgaaat agaacaactg caggctcaga 1350
 tccggaacct gaccgtgctg acccccgaag gggaggcagg gctgagctgg 1400
 cccgttgggc tccctgctcc ttccacacca cactctcgct ttgaggtgct 1450
 gggctgggac tacttcacag agcagcacac cttctcctgt gcagatgggg 1500
 ctcccaagtg cccactacag ggggctagca gggcggacgt ggggtgatgcg 1550
 ttggagactg ccctggagca gctcaatcgg cgctatcagc cccgcctgcg 1600
 cttccagaag cagcgactgc tcaacggcta tcggcgcttc gaccagcac 1650
 ggggcatgga gtacacctg gacctgctgt tggaatgtgt gacacagcgt 1700
 gggcacccgc gggccctggc tcgcagggtc agcctgctgc ggccactgag 1750
 ccgggtggaa atcctaccta tgccctatgt cactgaggcc acccgagtgc 1800
 agctgggtgct gccactcctg gtggctgaag ctgctgcagc cccggctttc 1850
 ctcgaggcgt ttgcagccaa tgtcctggag ccacgagaac atgcattgct 1900
 caccctgttg ctggtctacg ggccacgaga aggtggccgt ggagctccag 1950
 acccatttct tggggtgaag gctgcagcag cggagttaga gcgacggtac 2000
 cctgggacga ggctggcctg gctcgctgtg cgagcagagg ccccttccca 2050
 ggtgcgactc atggacgtgg tctcgaagaa gcaccctgtg gacactctct 2100

	95		100		105
Val Leu Thr Ser	Arg Ala Thr Leu Ser	Thr Leu Ala Val	Ala Val		
	110		115		120
Asn Arg Thr Val	Ala His His Phe Pro	Arg Leu Leu Tyr	Phe Thr		
	125		130		135
Gly Gln Arg Gly	Ala Arg Ala Pro Ala	Gly Met Gln Val	Val Ser		
	140		145		150
His Gly Asp Glu	Arg Pro Ala Trp Leu	Met Ser Glu Thr	Leu Arg		
	155		160		165
His Leu His Thr	His Phe Gly Ala Asp	Tyr Asp Trp Phe	Phe Ile		
	170		175		180
Met Gln Asp Asp	Thr Tyr Val Gln Ala	Pro Arg Leu Ala	Ala Leu		
	185		190		195
Ala Gly His Leu	Ser Ile Asn Gln Asp	Leu Tyr Leu Gly	Arg Ala		
	200		205		210
Glu Glu Phe Ile	Gly Ala Gly Glu Gln	Ala Arg Tyr Cys	His Gly		
	215		220		225
Gly Phe Gly Tyr	Leu Leu Ser Arg Ser	Leu Leu Leu Arg	Leu Arg		
	230		235		240
Pro His Leu Asp	Gly Cys Arg Gly Asp	Ile Leu Ser Ala	Arg Pro		
	245		250		255
Asp Glu Trp Leu	Gly Arg Cys Leu Ile	Asp Ser Leu Gly	Val Gly		
	260		265		270
Cys Val Ser Gln	His Gln Gly Gln Gln	Tyr Arg Ser Phe	Glu Leu		
	275		280		285
Ala Lys Asn Arg	Asp Pro Glu Lys Glu	Gly Ser Ser Ala	Phe Leu		
	290		295		300
Ser Ala Phe Ala	Val His Pro Val Ser	Glu Gly Thr Leu	Met Tyr		
	305		310		315
Arg Leu His Lys	Arg Phe Ser Ala Leu	Glu Leu Glu Arg	Ala Tyr		
	320		325		330
Ser Glu Ile Glu	Gln Leu Gln Ala Gln	Ile Arg Asn Leu	Thr Val		
	335		340		345
Leu Thr Pro Glu	Gly Glu Ala Gly Leu	Ser Trp Pro Val	Gly Leu		
	350		355		360

Pro	Ala	Pro	Phe	Thr	Pro	His	Ser	Arg	Phe	Glu	Val	Leu	Gly	Trp	365	370	375
Asp	Tyr	Phe	Thr	Glu	Gln	His	Thr	Phe	Ser	Cys	Ala	Asp	Gly	Ala	380	385	390
Pro	Lys	Cys	Pro	Leu	Gln	Gly	Ala	Ser	Arg	Ala	Asp	Val	Gly	Asp	395	400	405
Ala	Leu	Glu	Thr	Ala	Leu	Glu	Gln	Leu	Asn	Arg	Arg	Tyr	Gln	Pro	410	415	420
Arg	Leu	Arg	Phe	Gln	Lys	Gln	Arg	Leu	Leu	Asn	Gly	Tyr	Arg	Arg	425	430	435
Phe	Asp	Pro	Ala	Arg	Gly	Met	Glu	Tyr	Thr	Leu	Asp	Leu	Leu	Leu	440	445	450
Glu	Cys	Val	Thr	Gln	Arg	Gly	His	Arg	Arg	Ala	Leu	Ala	Arg	Arg	455	460	465
Val	Ser	Leu	Leu	Arg	Pro	Leu	Ser	Arg	Val	Glu	Ile	Leu	Pro	Met	470	475	480
Pro	Tyr	Val	Thr	Glu	Ala	Thr	Arg	Val	Gln	Leu	Val	Leu	Pro	Leu	485	490	495
Leu	Val	Ala	Glu	Ala	Ala	Ala	Ala	Pro	Ala	Phe	Leu	Glu	Ala	Phe	500	505	510
Ala	Ala	Asn	Val	Leu	Glu	Pro	Arg	Glu	His	Ala	Leu	Leu	Thr	Leu	515	520	525
Leu	Leu	Val	Tyr	Gly	Pro	Arg	Glu	Gly	Gly	Arg	Gly	Ala	Pro	Asp	530	535	540
Pro	Phe	Leu	Gly	Val	Lys	Ala	Ala	Ala	Ala	Glu	Leu	Glu	Arg	Arg	545	550	555
Tyr	Pro	Gly	Thr	Arg	Leu	Ala	Trp	Leu	Ala	Val	Arg	Ala	Glu	Ala	560	565	570
Pro	Ser	Gln	Val	Arg	Leu	Met	Asp	Val	Val	Ser	Lys	Lys	His	Pro	575	580	585
Val	Asp	Thr	Leu	Phe	Phe	Leu	Thr	Thr	Val	Trp	Thr	Arg	Pro	Gly	590	595	600
Pro	Glu	Val	Leu	Asn	Arg	Cys	Arg	Met	Asn	Ala	Ile	Ser	Gly	Trp	605	610	615
Gln	Ala	Phe	Phe	Pro	Val	His	Phe	Gln	Glu	Phe	Asn	Pro	Ala	Leu	620	625	630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp
 635 640 645
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile
 650 655 660
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr
 665 670 675
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu
 680 685 690
 Ala Gly Gln Glu Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met
 695 700 705
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val
 710 715 720
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro
 725 730 735
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu
 740 745 750
 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu
 755 760 765
 Gln Glu Gln Ala Asn Ser Thr
 770

<210> 340

<211> 1572

<212> DNA

<213> Homo Sapien

<400> 340

cggagtgggtg cgccaacgtg agaggaaacc cgtgcgcggc tgcgctttcc 50
 tgtccccaag ccgttctaga cgcgggaaaa atgctttctg aaagcagctc 100
 ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150
 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200
 catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250
 ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300
 ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350
 accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000

gtttgagtca attaatatgg acacaaatga catgtgggta atgatgagaa 450
 aagcttaciaa atacgccttt gataagtata gagaccaata caactgggtc 500
 ttccttgacac gcccactac gtttgctatc attgaaaacc taaagtattt 550
 tttgttaaaa aaggatccat cacagccttt ctatctaggc cacactataa 600
 aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650
 gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700
 tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750
 cagtttgcct gaaatatgct ggagtatttg cagaaaatgc agaagatgct 800
 gatggaaaag atgtatttaa taccaaatct gttgggcttt ctattaaaga 850
 ggcaatgact tatcaccoca accaggtagt agaaggctgt tgttcagata 900
 tggtctgttac ttttaatgga ctgactccaa atcagatgca tgtgatgatg 950
 tatgggggtat accgccttag ggcatttggg catattttca atgatgcatt 1000
 ggtttttotta cctccaaatg gttctgacaa tgactgagaa gtggtagaaa 1050
 agcgtgaata tgatctttgt ataggacgtg tgttgtcatt atttgtagta 1100
 gtaactacat atccaatata gctgtatggt tctttttctt ttctaatttg 1150
 gtggcactgg tataaccaca cattaaagtc agtagtacat ttttaaatga 1200
 ggggtggtttt tttcttttaa acacatgaac attgtaaatg tgttggaag 1250
 aagtgtttta agaataataa ttttgcaa ataaactattaa taaatattat 1300
 atgtgataaa ttctaaatta tgaacattag aaatctgtgg ggcacatatt 1350
 tttgctgatt ggtaaaaaa ttttaacagg tcttttagcgt tctaagatat 1400
 gcaaatgata tctctagttg tgaatttggt attaaagtaa aacttttagc 1450
 tgtgtgttcc ctttacttct aatactgatt tatgtttctaa gcctcccaa 1500
 gttccaatgg atttgccttc tcaaaatgta caactaagca actaaagaaa 1550
 attaaagtga aagttgaaaa at 1572

<210> 341

<211> 318

<212> PRT

<213> Homo Sapien

F
 A
 M
 I
 L
 Y
 N
 A
 M
 E
 S
 A
 R
 E
 L
 I
 S
 T
 E
 D
 I
 N
 T
 H
 I
 S
 F
 I
 L
 E
 A
 T
 E

<400> 341

Met	Leu	Ser	Glu	Ser	Ser	Ser	Phe	Leu	Lys	Gly	Val	Met	Leu	Gly
1				5					10					15
Ser	Ile	Phe	Cys	Ala	Leu	Ile	Thr	Met	Leu	Gly	His	Ile	Arg	Ile
				20					25					30
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln
				35					40					45
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg
				50					55					60
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val
				65					70					75
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp
				80					85					90
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val
				95					100					105
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu
				110					115					120
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp
				125					130					135
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile
				140					145					150
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln
				155					160					165
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr
				170					175					180
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys
				185					190					195
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln
				200					205					210
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val
				215					220					225
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala
				230					235					240
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile
				245					250					255
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys

PUB-400-341

	260		265		270
Cys Ser Asp Met	Ala Val Thr Phe Asn Gly	Leu Thr Pro Asn Gln			
	275		280		285
Met His Val Met	Met Tyr Gly Val Tyr Arg	Leu Arg Ala Phe Gly			
	290		295		300
His Ile Phe Asn	Asp Ala Leu Val Phe Leu	Pro Pro Asn Gly Ser			
	305		310		315

Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

tccccaagcc gttctagacg cgg 23

<210> 343

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctggttccttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 344

gcccaaattgc cctaaggcgg tatacccc 28

<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

<223> Synthetic Oligonucleotide Probe

<400> 345

gggtgtgatg cttggaagca ttttctgtgc tttgatcact atgctaggac 50

<210> 346

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 346

gggatgcagg tgggtgtctca tgggg 25

<210> 347

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 347

ccctcatgta ccggctcc 18

<210> 348

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 348

ggattctaatac gactcact atagggctca gaaaagcgca acagagaa 48

<210> 349

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 349

ctatgaaatt aaccctcact aaagggatgt cttccatgcc aaccttc 47

<210> 350

<211> 48

<212> DNA

<213> Artificial Sequence

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2015. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

<220>
<223> Synthetic Oligonucleotide Probe

<400> 350
ggattctaatacgcactcactatagggcgccgatgtccactggggctac 48

<210> 351
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 351
ctatgaaattaacccctcactaaagggacgaggaagatgggcggatgggt 48

<210> 352
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 352
ggattctaatacgcactcactatagggcaccacgcgtccggctgctt 47

<210> 353
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 353
ctatgaaattaacccctcactaaagggacggggacaccacggaccaga 48

<210> 354
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 354
ggattctaatacgcactcactatagggcttgctgcgggttttggttcctg 48

<210> 355
<211> 48

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 355
 ctatgaaatt aaccctcact aaaggagct gccgatccca ctggtatt 48

 <210> 356
 <211> 46
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 356
 ggattctaatacgcactcact atagggcgga tcctggccgg cctctg 46

 <210> 357
 <211> 48
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 357
 ctatgaaatt aaccctcact aaaggagcc cgggcatggt ctcagtta 48

 <210> 358
 <211> 47
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 358
 ggattctaatacgcactcact atagggcggg aagatggcga ggaggag 47

 <210> 359
 <211> 48
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 359
 ctatgaaatt aaccctcact aaagggacca aggccacaaa cggaaatc 48

<210> 360
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 360
ggattctaatacgaactcactatagggctgtgctttcattctgccagta 48

<210> 361
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 361
ctatgaaattaacccctcactaaagggaggggtacaattaagggtggat 48

<210> 362
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 362
ggattctaatacgaactcactatagggcccgctcgtcctgctcctg 47

<210> 363
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 363
ctatgaaattaacccctcactaaagggaggaatgccgcgacctcacag 48

<210> 364
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 364

ggattctaatac gactcact atagggcccc tctgccttc cctgtcc 47

<210> 365

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 365

ctatgaaatt aaccctcact aaaggagggtg gtggccgcga ttatctgc 48

<210> 366

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 366

ggattctaatac gactcact atagggcgca gcatggcag cgatgagg 48

<210> 367

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 367

ctatgaaatt aaccctcact aaagggacag acggggcaga gggagtgc 47

<210> 368

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 368

ggattctaatac gactcact atagggccag gaggcgtgag gagaaac 47

<210> 369

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 369

ctatgaaatt aaccctcact aaagggaaag acatgtcatc gggagtgg 48

<210> 370

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 370

ggattctaatt acgactcact atagggccgg gtggaggtgg aacagaaa 48

<210> 371

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 371

ctatgaaatt aaccctcact aaagggacac agacagagcc ccatacgc 48

<210> 372

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 372

ggattctaatt acgactcact atagggccag ggaaatccgg atgtctc 47

<210> 373

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 373

ctatgaaatt aaccctcact aaagggagta aggggatgcc accgagta 48

<210> 374

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 374

ggatttcta atc gactcact atagggccag ctacccgcag gaggagg 47

<210> 375

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 375

ctatgaaatt aaccctcact aaagggatcc cagggtgatga ggtccaga 48

<210> 376

<211> 997

<212> DNA

<213> Homo Sapien

<400> 376

cccacgcgtc cgatcttacc aacaaaacac tcttgaggag aaagaaagag 50
 agggagggag agaaaaagag agagagagaa acaaaaaacc aaagagagag 100
 aaaaaatgaa ttcattctaaa tcatctgaaa cacaatgcac agagagagga 150
 tgcttctctt cccaaatgtt cttatggact gttgctggga tccccatcct 200
 atttctcagt gcctgtttca tcaccagatg tggtgtgaca tttcgcatct 250
 ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300
 ctctcctgct acaattatgg atcagggttca gtcaagaatt gttgtccatt 350
 gaactgggaa tattttcaat ccagctgcta cttcttttct actgacacca 400
 tttcctgggc gttaagttaa aagaactgct cagccatggg ggctcacctg 450
 gtggttatca actcacagga ggagcaggaa ttcctttcct acaagaaacc 500
 taaaatgaga gagtttttta ttggactgtc agaccagggtt gtcgaggggtc 550
 agtggcaatg ggtggacggc acacctttga caaagtctct gagcttctgg 600
 gatgtagggg agcccaacaa catagctacc ctggaggact gtgccaccat 650
 gagagactct tcaaacccaa ggcaaaattg gaatgatgta acctgtttcc 700
 tcaattatct tcggatttgt gaaatggtag gaataaatcc tttgaacaaa 750

ggaaaatctc ttttaagaaca gaaggcacaa ctcaaattgtg taaagaagga 800
 agagcaagaa catggccaca cccaccgccc cacacgagaa atttgtgcgc 850
 tgaacttcaa aggacttcat aagtatttgt tactctgata caaataaaaa 900
 taagtagttt taaatgttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 950
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 997

<210> 377

<211> 219

<212> PRT

<213> Homo Sapien

<400> 377

Met	Asn	Ser	Ser	Lys	Ser	Ser	Glu	Thr	Gln	Cys	Thr	Glu	Arg	Gly
1				5					10					15
Cys	Phe	Ser	Ser	Gln	Met	Phe	Leu	Trp	Thr	Val	Ala	Gly	Ile	Pro
				20					25					30
Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr
				35					40					45
Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro
				50					55					60
Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser
				65					70					75
Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser
				80					85					90
Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu
				95					100					105
Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser
				110					115					120
Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg
				125					130					135
Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp
				140					145					150
Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp
				155					160					165
Asp	Val	Gly	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala
				170					175					180

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400

<210> 382
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 382
ggccttgacg acaaccgt 18

<210> 383
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 383
cagactgagg gagatccgag a 21

<210> 384
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 384
cagctgccct tccccaaacca 20

<210> 385
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 385
catcaagcgc ctctacca 18

<210> 386
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 386

FBI LABORATORY

```
<210> 387
<211> 18
<212> DNA
<213> Artificial Sequence
```

```
<400> 387
  gggccatcac agctccct 18
```

<220>
<223> Synthetic oligonucleotide probe

```
<210> 389
<211> 22
```

<220>
<223> Synthetic oligonucleotide probe

```
<210> 390
<211> 20
<212> DNA
<213> Artificial Sequence
```

<400> 390
cagaaggatg tcccgtggaa 20

<220>

<223> Synthetic oligonucleotide probe

<400> 391

gccgctgtcc actgcag 17

<210> 392

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

gacggcatcc tcagggccac a 21

<210> 393

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

atgtcctcca tgcccacgcg 20

<210> 394

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 394

gagtgcgaca tcgagagctt 20

<210> 395

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 395

ccgcagcctc agtgatga 18

<210> 396

<211> 21

<212> DNA

<213> Artificial Sequence

<210> 401
<211> 29

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 401
cacagagcat ttgtccatca gcagttcag 29

<210> 402
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 402
ggcagagact tccagtcact ga 22

<210> 403
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 403
gccaaagggtg gtgtagata gg 22

<210> 404
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 404
caggccccct tgatctgtac ccca 24

<210> 405
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 405
gggacgtgct tctacaagaa cag 23

<210> 406
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 406
caggcttaca atgttatgat cagaca 26

<210> 407
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 407
tattcagagt ttccattgg cagtgccagt t 31

<210> 408
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 408
tctacatcag cctctctgcg c 21

<210> 409
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 409
cgatcttctc caccaggag cgg 23

<210> 410
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 410


```
<210> 411
<211> 23
<212> DNA
<213> Artificial Sequence
```

```
<400> 411
ctccctgaat ggcagcctga gca 23
```

<212> DNA
<213> Artificial Sequence

```
<400> 412
aggtgtttat taagggccta cgct 24
```

<220>
<223> Synthetic oligonucleotide probe

<400> 413
cagagcagag ggtgccttg 19

```
<210> 414
<211> 21
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Synthetic oligonucleotide probe

```
<400> 414
  tggcggagtc ccctcttggc t 21
```

```
<210> 415
<211> 22
<212> DNA
<213> Artificial Sequence
```

<220>

<223> Synthetic oligonucleotide probe

<400> 415

ccctgtttcc ctatgcatca ct 22

<210> 416

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 416

tcaaccctg accctttcct a 21

<210> 417

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 417

ggcaggggac aagccatctc tcct 24

<210> 418

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

gggactgaac tgccagcttc 20

<210> 419

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 419

gggccctaac ctcattacct tt 22

<210> 420

<211> 23

<212> DNA

<213> Artificial Sequence

Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 420

tgtctgcctc agccccagga agg 23

<210> 421

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

tctgtccacc atcttgctt g 21

<210> 422

<211> 3554

<212> DNA

<213> Homo Sapien

<400> 422

gggactacaa gccgcgccgc gctgccgctg gccctcagc aaccctcgac 50
 atggcgctga ggcggccacc gcgactccgg ctctgcgctc ggctgcctga 100
 cttcttctctg ctgctgcttt tcaggggctg cctgataggg gctgtaaatc 150
 tcaaattccag caatcgaacc ccagtggtag aggaatttga aagtgtggaa 200
 ctgtcttgca tcattacgga ttcgcagaca agtgacccca ggatcgagt 250
 gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300
 ttcaggggaga cttggcgggt cgtgcagaaa tactggggaa gacatccctg 350
 aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt 400
 cgttgctcga aatgaccgca aggaaattga tgagatttg atcgagttaa 450
 ctgtgcaagt gaagccagt acccctgtct gtagagtgcc gaaggctgta 500
 ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550
 ccggcctcac tacagctggt atcgcaatga tgtaccactg cccacggatt 600
 ccagagccaa tcccagattt cgcaattctt ctttccactt aaactctgaa 650
 acaggcactt tgggtgttcac tgctgttcac aaggacgact ctgggcagta 700
 ctactgcatt gcttccaatg acgcaggctc agccagggtg gaggagcagg 750

1. 2. 3. 4. 5. 6. 7. 8. 9. 10. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100.

agatggaagt ctatgacctg aacattggcg gaattattgg gggggttctg 800
 gttgtccttg ctgtactggc cctgatcacg ttgggcatct gctgtgcata 850
 cagacgtggc tacttcatca acaataaaca ggatggagaa agttacaaga 900
 acccagggaa accagatgga gttaactaca tccgcaactga cgaggagggc 950
 gacttcagac acaagtcacg gtttgtgatc tgagaccgcg ggtgtggctg 1000
 agagcgcaca gagcgcacgt gcacatacct ctgctagaaa ctctgtcaa 1050
 ggcagcgaga gctgatgcac tcggacagag ctagacactc attcagaagc 1100
 ttttcgtttt ggccaaagtt gaccactact cttcttactc taacaagcca 1150
 catgaataga agaattttcc tcaagatgga cccggtaaata ataaccacaa 1200
 ggaagcgaaa ctgggtgcgt tcaactgagtt gggttcctaa tctgtttctg 1250
 gcctgattcc cgcattgagta ttagggatgat cttaaagagt ttgctcacgt 1300
 aaacgcccgt gctgggccct gtgaagccag catgttcacc actggctggt 1350
 cagcagccac gacagcacca tgtgagatgg cgagggtggc ggacagcacc 1400
 agcagcgcct cccggcgagg acccagaaaa ggcttcttac acagcagcct 1450
 tacttcatcg gccacagac accaccgcag tttcttctta aaggctctgc 1500
 tgatcgggtg tgcagtgtcc attgtggaga agctttttgg atcagcattt 1550
 tgtaaaaaca accaaaatca ggaaggtaaa ttggttgctg gaagagggat 1600
 cttgcctgag gaacctgct tgtccaacag ggtgtcagga ttttaaggaa 1650
 accttcgtct taggctaagt ctgaaatggc actgaaatat gcttttctat 1700
 gggctctgtt tattttataa aattttacat cttaaatttt gctaaggatg 1750
 tattttgatt attgaaaaga aaatttctat ttaaactgta aatatattgt 1800
 catacaatgt taaataacct atttttttta aaaagttcaa cttaaggtag 1850
 aagttccaag ctactagtgt taaattggaa aatatcaata attaagagta 1900
 ttttaoccaa ggaatcctct catggaagtt tactgtgatg ttccttttct 1950
 cacacaagtt ttagcctttt tcacaaggga actcatactg tctacacatc 2000
 agaccatagt tgcttaggaa accttttaaa attccagtta agcaatggtg 2050

aaatcagttt gcattcttctc aaaagaaacc tctcaggtta gctttgaact 2100
 gcctcttctc gagatgacta ggacagtctg taccagagg ccaccagaa 2150
 gccctcagat gtacatacac agatgccagt cagctcctgg ggttgccca 2200
 ggcccccgc ctctagctca ctggtgcctc gctgtctgcc aggaggccct 2250
 gccatccttg ggccctggca gtggtctgtg ccagtgagc ttactcacg 2300
 tggcccttgc ttcattccagc acagctctca ggtgggcact gcaggacac 2350
 tgggtgtctc catgtagcgt ccagctttg ggctcctgta acagacctct 2400
 ttttggttat ggatggctca caaataggg ccccaatgc tatttttttt 2450
 ttttaagttt gtttaattat ttgttaagat tgtctaaggc caaaggcaat 2500
 tgcgaaatca agtctgtcaa gtacaataac atttttaaaa gaaaatggat 2550
 cccactgttc ctctttgcca cagagaaagc acccagacgc cacaggctct 2600
 gtgcgatttc aaaacaaacc atgatggagt ggcggccagt ccagcctttt 2650
 aaagaacgtc aggtggagca gccaggtgaa aggcctggcg gggaggaaa 2700
 tgaaacgcct gaatcaaaag cagttttcta attttgactt taaatttttc 2750
 atccgccgga gacactgctc ccatttgtgg ggggacatta gcaacatcac 2800
 tcagaagcct gtgttcttca agagcagggtg ttctcagcct cacatgccct 2850
 gccgtgctgg actcaggact gaagtgtgt aaagcaagga gctgctgaga 2900
 aggagcactc cactgtgtgc ctggagaatg gctctcacta ctcacctgt 2950
 ctttcagctt ccagtgtctt gggtttttta tactttgaca gctttttttt 3000
 aattgcatac atgagactgt gttgactttt tttagttatg tgaaacactt 3050
 tgccgcaggc cgctggcag aggcaggaaa tgctccagca gtggctcagt 3100
 gctccctggg gtctgtgca tggcatcctg gatgcttagc atgcaagttc 3150
 cctccatcat tgccaccttg gtagagaggg atggctccc accctcagcg 3200
 ttggggattc acgctccagc ctcttcttgg gttgtcatag tgatagggt 3250
 gccttattgc cccctcttct tataccctaa aaccttctac actagtcca 3300
 tgggaaccag gtctgaaaaa gtagagagaa gtgaaagtag agtctgggaa 3350
 gtagctgcct ataactgaga ctagacggaa aaggaaact cgtgtatttt 3400

```
<210> 423
<211> 310
<212> PRT
<213> Homo Sapien
```

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Arg | Arg | Pro | Pro | Arg | Leu | Arg | Leu | Cys | Ala | Arg | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |
| Pro | Asp | Phe | Phe | Leu | Leu | Leu | Leu | Phe | Arg | Gly | Cys | Leu | Ile | Gly |
| | | | | 20 | | | | | 25 | | | | | 30 |
| Ala | Val | Asn | Leu | Lys | Ser | Ser | Asn | Arg | Thr | Pro | Val | Val | Gln | Glu |
| | | | | 35 | | | | | 40 | | | | | 45 |
| Phe | Glu | Ser | Val | Glu | Leu | Ser | Cys | Ile | Ile | Thr | Asp | Ser | Gln | Thr |
| | | | | 50 | | | | | 55 | | | | | 60 |
| Ser | Asp | Pro | Arg | Ile | Glu | Trp | Lys | Lys | Ile | Gln | Asp | Glu | Gln | Thr |
| | | | | 65 | | | | | 70 | | | | | 75 |
| Thr | Tyr | Val | Phe | Phe | Asp | Asn | Lys | Ile | Gln | Gly | Asp | Leu | Ala | Gly |
| | | | | 80 | | | | | 85 | | | | | 90 |
| Arg | Ala | Glu | Ile | Leu | Gly | Lys | Thr | Ser | Leu | Lys | Ile | Trp | Asn | Val |
| | | | | 95 | | | | | 100 | | | | | 105 |
| Thr | Arg | Arg | Asp | Ser | Ala | Leu | Tyr | Arg | Cys | Glu | Val | Val | Ala | Arg |
| | | | | 110 | | | | | 115 | | | | | 120 |
| Asn | Asp | Arg | Lys | Glu | Ile | Asp | Glu | Ile | Val | Ile | Glu | Leu | Thr | Val |
| | | | | 125 | | | | | 130 | | | | | 135 |
| Gln | Val | Lys | Pro | Val | Thr | Pro | Val | Cys | Arg | Val | Pro | Lys | Ala | Val |
| | | | | 140 | | | | | 145 | | | | | 150 |
| Pro | Val | Gly | Lys | Met | Ala | Thr | Leu | His | Cys | Gln | Glu | Ser | Glu | Gly |
| | | | | 155 | | | | | 160 | | | | | 165 |
| His | Pro | Arg | Pro | His | Tyr | Ser | Trp | Tyr | Arg | Asn | Asp | Val | Pro | Leu |
| | | | | 170 | | | | | 175 | | | | | 180 |
| Pro | Thr | Asp | Ser | Arg | Ala | Asn | Pro | Arg | Phe | Arg | Asn | Ser | Ser | Phe |
| | | | | 185 | | | | | 190 | | | | | 195 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Leu | Asn | Ser | Glu | Thr | Gly | Thr | Leu | Val | Phe | Thr | Ala | Val | His |
| | | | | 200 | | | | | 205 | | | | | 210 |
| Lys | Asp | Asp | Ser | Gly | Gln | Tyr | Tyr | Cys | Ile | Ala | Ser | Asn | Asp | Ala |
| | | | | 215 | | | | | 220 | | | | | 225 |
| Gly | Ser | Ala | Arg | Cys | Glu | Glu | Gln | Glu | Met | Glu | Val | Tyr | Asp | Leu |
| | | | | 230 | | | | | 235 | | | | | 240 |
| Asn | Ile | Gly | Gly | Ile | Ile | Gly | Gly | Val | Leu | Val | Val | Leu | Ala | Val |
| | | | | 245 | | | | | 250 | | | | | 255 |
| Leu | Ala | Leu | Ile | Thr | Leu | Gly | Ile | Cys | Cys | Ala | Tyr | Arg | Arg | Gly |
| | | | | 260 | | | | | 265 | | | | | 270 |
| Tyr | Phe | Ile | Asn | Asn | Lys | Gln | Asp | Gly | Glu | Ser | Tyr | Lys | Asn | Pro |
| | | | | 275 | | | | | 280 | | | | | 285 |
| Gly | Lys | Pro | Asp | Gly | Val | Asn | Tyr | Ile | Arg | Thr | Asp | Glu | Glu | Gly |
| | | | | 290 | | | | | 295 | | | | | 300 |
| Asp | Phe | Arg | His | Lys | Ser | Ser | Phe | Val | Ile | | | | | |
| | | | | 305 | | | | | 310 | | | | | |

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000